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(54) Title: **DIAGNOSIS AND TREATMENT METHODS RELATED TO AGING, ESPECIALLY IN MUSCLE (14.1)**

(57) Abstract: Mouse genes differentially expressed in comparisons of gene expression in different ages of mouse muscles have been identified, as have corresponding human genes and proteins. The human molecules, or antagonists thereof, may be used for protection against faster-than-normal biological aging, or to achieve slower-than-normal biological aging. The human molecules may also be used as markers of biological aging.



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DIAGNOSIS AND TREATMENT METHODS RELATED TO AGING, ESPECIALLY
IN MUSCLE (14.1)

Cross-Reference to Related Applications

Anti-Aging Applications. Mice with a disrupted growth hormone receptor/binding protein gene enjoy an increased lifespan. In U.S. Prov. Appl. 60/485,222, filed July 8, 2003 (Kopchick8) mouse genes differentially expressed in comparisons of gene expression in growth hormone receptor/binding protein gene-disrupted mouse livers and normal mouse livers were identified, as were corresponding human genes and proteins. It was suggested that the human molecules, or antagonists thereof, could be used for protection against faster-than-normal biological aging, or to achieve slower-than-normal biological aging. It was also taught that the human molecules may also be used as markers of biological aging.

In provisional application Ser. No. 60/474,606, filed June 2, 2003 (our docket Kopchick7-USA) , our research group used a gene chip to study the genetic changes in the liver of C57Bl/6J mice that occur at frequent intervals of the aging process. Differential hybridization techniques were used to identify mouse genes that are differentially expressed in mice, depending upon their age. The level of gene expression of approximately 10,000 mouse genes (from the Amersham Codelink UniSet Mouse I Bioarray, product code: 300013) in the liver of mice with average ages of 35, 49, 56, 77, 118, 133, 207, 403, 558 and 725 days was determined. In essence, complementary RNA derived from mice of different ages was screened for hybridization with oligonucleotide probes each specific to a particular mouse gene, each gene in turn representative of a particular mouse gene cluster (Unigene). Mouse genes which were differentially expressed (younger vs. older), as measured by different levels of hybridization of the respective cRNA

samples with the particular probe corresponding to that mouse gene, were identified. Related human genes and proteins were identified by sequence comparisons to the mouse gene or protein. In the international appl. Kopchick7A-PCT, filed June 2, 2004, we added some additional studies of CIDE-A (see below).

In a like manner, the effect of aging on the expression of genes in mouse skeletal muscle was studied, see provisional application Ser. No. 60/566,068, filed April 29, 2004 (our docket Kopchick14-USA).

Anti-Diabetes Applications. In U.S. Provisional Appl. Ser. No. 60/458,398 (our docket Kelder1-USA), filed March 31, 2003, members of our research group describe the identification of genes differentially expressed in normal vs. hyperinsulinemic, hyperinsulinemic vs. type II diabetic, or normal vs. type II diabetic mouse liver. Forward- and reverse-subtracted cDNA libraries were prepared, clones were isolated, and differentially expressed cDNA inserts were sequenced and compared with sequences in publicly available sequence databases. The corresponding mouse and human genes and proteins were identified.

The purpose of our research group's provisional application Ser. No. 60/460,415 (our docket: Kopchick6-USA), filed April 7, 2003, was similar, but complementary RNA, derived from RNA of mouse liver, was screened against a mouse gene chip. See also 60/506,716, filed Sept. 30, 2003 (Kopchick6.1).

Gene chip analyses have also been used to identify genes differentially expressed in normal vs. hyperinsulinemic, hyperinsulinemic vs. type II diabetic, or normal vs. type II diabetic mouse pancreas, see U.S. Provisional Appl. 60/517,376, filed Nov. 6, 2003

(Kopchick12) and **muscle**, see U.S. Provisional Appl. 60/547,512, filed Feb. 26, 2004 (Kopchick15).

Other differential hybridization applications. The use of differential hybridization to identify genes and proteins is also described in our research group's Ser. No. PCT/US00/12145 (Kopchick 3A-PCT), Ser. No. PCT/US00/12366 (Kopchick4A-PCT), and Ser. No. 60/400,052 (Kopchick5).

All of the foregoing applications are hereby incorporated by reference in their entirety.

BACKGROUND OF THE INVENTIONField of the Invention

The invention relates to various nucleic acid molecules and proteins, and their use in (1) diagnosing aging, or adverse conditions associated with the aging process, and (2) protecting mammals (including humans) against the aging process or adverse conditions associated with the aging process.

Description of the Background Art

The mechanisms that cause aging (the decline in survival and reproductive ability with advancing age) have puzzled our society and scientific community for centuries. The two major theories center on the question of whether normal aging is an evolutionarily-genetically preprogrammed pathway of internal changes or is a normal consequence of existence where there is an accumulation of molecular and cellular damages. Hypotheses of such accumulated damage include free radical-oxidative damage, defective mitochondria, somatic mutations, progressive shortening of telomeres, programmed cell death, impaired cell proliferation and numerous others (1). The current belief is that aging is not a programmed process in that, to date, no genes are known to have evolved specifically to cause damage and aging. The one factor that has been shown to extend the lifespan in organisms from yeast to mice has been a reduction in caloric intake (2, 3). Recent data suggests that caloric restriction may also be relevant for primates, including humans (4-6). Unfortunately, it is unlikely that most people will be able to maintain the strict dietary control required to reap the benefits of this finding. Therefore, since the mechanism(s) by which caloric restriction extends lifespan are unknown, the elucidation of

such mechanisms could lead to the development of alternative strategies to yield similar benefits.

Numerous groups are presently engaged in identifying genes and pathways that are involved in the aging process. A growing list of genes that extend adult longevity have been identified and a large proportion of these genes are involved with hormonal signals. Many of these genes and the corresponding endocrine systems are conserved among a wide variety of eukaryotes. What is becoming clear, at least in lower animal species, is that those pathways that provide advantages to development and growth early in life may impart negative consequences in later life. The clearest example of a genetic pathway affecting adult lifespan has been described in the nematode, *Caenorhabditis elegans*.

When food is abundant, *C. elegans* develops directly to the reproductive adult through four larval stages in three days. Under adverse conditions such as caloric restriction or high population density, *C. elegans* enters the Dauer diapause, a non-feeding, stress-resistant larval state. Genetic analysis has identified that mutation of single genes involved in dauer formation (*Daf*) greatly extend the adult lifespan (7). These genes involve the highly-conserved insulin/IGF-like signal transduction pathway. Ligand binding to the *daf-2* insulin-like receptor results in a kinase signaling cascade to phosphorylate the forkhead transcription factor, *daf-16*. This phosphorylation sequesters *daf-16* to the cytoplasm and results in reproductive maturity and aging. In the absence of ligand and signal transduction, the unphosphorylated, *daf-16* localizes to the nucleus and regulates the transcription of its target genes that promote dauer formation, stress resistance and extended longevity (8). A similar pathway has been described in *Drosophila melanogaster*. Mutation of the gene encoding insulin-like receptor (*InR*) or the gene

encoding insulin-receptor substrate (*chico*) also extends the normal life-span (9,10). Vertebrate homologues of *daf-16* down-regulate genes promoting cell progression, induce genes involved in DNA-damage repair and up-regulate genes that reduce intracellular reactive oxygen species (ROS) (11,12). A second *C. elegans* gene, *clk-1*, has also been linked to the reduction of ROS and an extended life-span. While the effect of *daf-2* mutants result in a reduction of mitochondrial ROS, *clk-1* mutants reduce extramitochondrially produced ROS. Since the majority of cellular ROS is produced in the mitochondria during the process of electron transport, it is not surprising that *clk-1* mutants have only a moderately extended life-span. *C. elegans* containing *daf-2/clk-1* double mutations, however, exhibit a very long life-span (13).

Decreased IGF-1 signaling may also extend longevity in mice. Four mouse models with deficiencies in pituitary endocrine action have demonstrated retarded aging. In the *Prop1* and *Pit1* models, pituitary production of growth hormone (GH), prolactin (PRL) and thyroid stimulating hormone (TSH) are ablated. These mice have reduced growth rates, reduced adult body size and live 40 to 60% longer than normal mice (14,15). Unfortunately, it is not possible to determine which of the ablated hormones is responsible for the increased longevity of the models.

A more straightforward model was developed that targeted the deletion of the growth hormone receptor (*GHR-KO*) (16). This mouse line was derived from a founder animal by homologous recombination resulting in deletion and gene substitution of most of the fourth exon and part of the fourth intron of the *GHR/BP* gene. These mice also exhibit reduced body size and extended life-span and more directly implicates the GH/IGF-1 axis (17, 17a).

Recently, evidence for a direct role of IGF-1 receptor signaling in affecting the aging process was provided by the targeted disruption of the IGF-1 receptor (*Igf1r*) (18). Heterozygous females, but not males, possess 50% fewer receptors for IGF-1, live 33% longer than wild-type females and also display greater resistance to oxidative stress. Tyrosine phosphorylation of the intracellular signaling molecule, *Shc*, was also decreased in the *Igf1r*^{+/-} females. Mice containing the targeted deletion of *p66shc* also have increased resistance to oxidative stress and a 30% increase in life span (19). While the IGF-1 axis appears to be involved in the aging process, the mechanism by which it does so remains unknown. However, these findings demonstrate that it is possible to identify specific genetic pathways that affect the aging process. The finding that caloric restriction of these mouse models can further extend their life-span suggests that multiple pathways exist that affect the aging process (20). Therefore, research to identify these pathways and the genes involved in the aging process is of great importance.

The role of growth hormone in aging is further discussed in Vance, ML, "Can Growth Hormone Prevent Aging," *New Engl. J. Med.*, 348: 779-80 (Feb. 27, 2003).

Gene Chip-Based Identification of genes involved in aging of skeletal muscle

Several groups have used DNA microarrays to measure differences in gene expression caused by the aging process. However, these experiments are extremely limited in regards to the number of aging time points or experimental conditions.

Weindruch, et al., "Microarray profiling of gene expression in aging and its alteration by caloric

restriction in mice" in Symposium: Calorie Restriction: effects on Body Composition, Insulin Signaling and Aging 918S-923S (2001) (21) compared expression in gastrocnemius muscle from 5- and 30-month old C57BL/6 mice, with and without caloric restriction. In this analysis, the expression of 113 genes was found to be changed by at least two-fold in 5-month old mice compared to 30-month old mice. Caloric restriction of comparable mice caused a reversal of the altered gene expression of 33 genes.

Of the 6347 genes surveyed in the oligonucleotide microarray, only 58 (0.9%) displayed a greater than 2 fold increase in gene expression as a function of aging, whereas 55(0.9%) displayed a greater than 2 fold decrease.

Of the genes positively correlated with aging, 16% could be assigned to stress responses. The largest differential expression between young and aged animals (3.8 fold) was the mitochondrial sarcomeric creatine kinase.

Of the genes negatively correlated with aging, 13% were involved in energy metabolism. A noteworthy number were genes encoding biosynthetic enzymes (cytochrome P450 IIC12, squalene synthase, stearyl-CoA desaturase, EF-1-gamma. Another down regulator was a CpG binding protein, MeCP2.

Weindruch further reported that age-related changes in gene expression profile were "remarkably attenuated" by caloric restriction.

What appears to be the same experiment is discussed in Lee, et al., "Gene expression profile of aging and its retardation by caloric restriction," Science, 285: 1390 (Aug. 27, 1999). This papers lists the individual genes which were differentially expressed by more than 2-fold, and classifies them as energy metabolism, neuronal factors, protein metabolism, stress response, biosynthesis, calcium metabolism or DNA repair genes.

Welle, et al., "Skeletal muscle gene expression profiles in 20-29 year old and 65-71 year old women," *Exper. Gerontol.*, 39: 369-77 (2004) and available electronically as doi:10.1016/j.exger.2003.11.011 studied gene expression and physical condition in seven young and eight older women. With respect to physical condition, the measured or calculated parameters were total body mass, lean body mass, left leg lean mass (by biopsy), maximum isometric left knee extension force, left knee extension force/left leg lean mass, Peak VO_2 /lean body mass, and Peak VO_2 /left leg lean mass.

There were 1178 "probe sets" (representing 1053 different Unigene clusters) for which differential expression was detected; 550 for which expression was higher in older women, and 628 the inverse effect. The differences ranged from 1.2 to 4 fold; most (78A%) were less than 1.5 fold. The complete list of differentially expressed genes is given in the Rochester Muscle database website, www.urmc.rochester.edu/smd/crc/swindex (".html" omitted, in accordance with USPTO requirements, so that the publication of this application will not create an active hyperlink).

The gene most highly overexpressed in older muscle was p21 (cyclin-dependent kinase inhibitor 1A) (4.01 fold). This one of several genes (see Welle Table 2) which are potentially related to DNA damage and repair. Welle also thought it noteworthy how many of the differentially expressed genes were ones that encode proteins which bind to pre-mRNAs or mRNAs (see Welle Table 3).

Gene-Chip Based Identification of Genes Involved in aging of other organs and tissues

Microarrays have also been used in the identification of aging-related genes by virtue of differential expression

in other organs and tissues, see, e.g., Miller, J. Gerontol., 56A: B52-57 (2001) (liver); Lee et al., Science, 285 :1390-93 (1999) and Nature Genetics 25: 294-7 (2000) (mouse cerebellum and neocortex); Lee et al., Proc Natl Acad Sci USA 99:14988-14993 (2002) (Ref. 22) (heart); Prolla, Chem Senses 27299-306 (2002) (Ref. 23) (brain).

Cao, S.X., et al., "Genomic profiling of short- and long-term caloric restriction effects in the liver of aging mice", Proc. Natl. Acad. Sci. USA, 98:10630-10635 (2001) used Affymetrix microarray technology to study the changes in expression levels of 11,000 genes in liver tissue of 7 month-old mice compared to 27 month-old mice. In this analysis, the expression of 20 genes increased at least 1.7-fold with age while the expression of 26 genes decreased at least 1.7-fold with age.

Tollet-Egnell, P., et al., "Gene expression profile of the aging process in rat liver: normalizing effects of growth hormone replacement, Mol. Endocrinol., 15(2):308-18 (2001) used microarray technology to study the effect of aging and growth hormone treatment on the expression of 3,000 different genes in the rat liver. The proteins which were over-expressed in the older rat were glucose-6-phosphate isomerase (x1.8), pyruvate kinase (x4.8), hepatic product spot 14 (2.4x), fatty acid synthase (1.9x), staryl CoA desaturase (1.7x), enoyl CoA hyydratase (1.7x), peroxisome proliferator activated receptor- α (1.7x), 3-ketoacyl-CoA thiolase (1.7x), 3-keto-acyl-CoA peroxisomal thiolase (1.9x), CYP4A3 (3.3x), glycerol-3-phosphate dehydrogenase (1.7x), NADPH-cytochrome P450 oxidoreductase (4.7x). CUP2C7 (1.9x), CYP3A2 (2.8x), Δ -aminoevulinate synthase (2.3x). The under-expressed proteins were glucose-6-phosphatase (0.3x), farnesyl pyrophosphate synthase (0.5x), carnitine octanoyltransferase (0.5x), mitochondrial genome (16S ribosomal RNA) (0.3x), mitochondrial cytochrome c

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oxidase II (0.4x), mitochondrial NADH dehydrogenase SU 5 (0.3x), mitochondrial cytochrome b (0.4x), mitochondrial NADH dehydrogenase SU 3 (0.5x), NADH-ubiquinone oxidoreductase (SU CI-SGDH and SU 39kDa) (both 0.5x), ubiquinol-cytochrome c reductase (Rieske iron-sulfur protein and core 1) (both 0.5x), CYP2C12 (0.4x), cystathione γ -lyase (0.3x), biphenyl hydrolase-related protein (0.5x), glutathione S-transferase (class pi) (0.3x), α -1 macroglobulin (0.5x), BRAK related protein (0.3x), α -2u-globulin (0.4x), cAMP-dependent transcription factor mATF4 (0.5x), DAP-like kinase (0.5x), PCTAIRE-1 (0.5x), collagen α -1 (0.4x), histone H2A (0.5x), and S-100 protein α (0.5x).

See also Dozmorov I, Bartke A, Miller RA., "Array-based expression analysis of mouse liver genes: effect of age and of the longevity mutant Prop1df", J. Gerontol., 56A: B52-57 (2001). Liver mRNA levels were measured in Ames dwarf mice (homozygous for the df allele at the Prop1 locus; live 40% to 70% longer than nonmutant siblings) and in control mice at ages 5, 13 and 22 months. "The analysis showed seven genes where the effects of age reach $p < .01$ in normal mice and six others with possible age effects in dwarf mice, but none of these met Bonferroni-adjusted significance thresholds. Thirteen genes showed possible effects of the df/df genotype at $p < .01$. One of these, insulin-like growth factor 1 (IGF-1), was statistically significant even after adjustment for multiple comparisons; and genes for two IGF-binding proteins, a cyclin, a heat shock protein, p38 mitogen-activated protein kinase, and an inducible cytochrome P450 were among those implicated by the survey. In young control mice, half of the expressed genes showed SDs that were more than 58% of the mean, and a simulation study showed that genes with this degree of interanimal variation would often produce false-positive findings when conclusions were based on ratio calculations alone (i.e.,

without formal significance testing). Many genes in our data set showed apparent young-to-old or normal-to-dwarf ratios above 2, but the large majority of these proved to be genes where high interanimal variation could create high ratios by chance alone, and only a few of the genes with large ratios achieved $p < .05$. The proportion of genes showing relatively large changes between 5 and 13 months, or from 13 to 22 months of age, was not diminished by the df/df genotype, providing no support for the idea that the dwarf mutation leads to global delay or deceleration of the pace of age-dependent changes in gene expression."

Other Anti-Aging Studies

For genes thought to have aging inhibitory activity, see generally International Longevity Center, Workshop Reports, "Longevity Genes: From Primitive Organisms to Humans," and "Is there an 'Anti-Aging' Medicine?".

Patents of possible interest include the following:

Lin, USP 6,303,768 (2001) ("Methuselah gene")

Lippman, USP 4,695,590 ("Method for retarding aging")

West, USP 6,368,789 (2002) ("Screening methods to identify inhibitors of telomerase activity")

Measurement of Biological Aging

Patents of possible interest include the following:

Kojima, USP 5,000,188 (1991) (an apparatus for measuring the physiological age of a subject).

Dimri, USP 5,795,728 (1998) ("Biomarkers of cell senescence")

Jia, USP 6,326,209 (2001) ("Measurement and quantification of 17 ketosteroid -sulfates as a biomarker of biological age")

Articles of interest include Kayo, et al., Proc. nat. Acad. Sci. (USA) 98:5093-98 (2001); Han, et al., Mch. Ageing Dev. 115:157-74 (2000); Dozmorov, et al., J. gerontol. A Biol. Sci. Med. Sci. 56:B72-B80 (2001); Dozmorov, et al., Id., 57: B99-B108 (2002); Miller, et al., Mol. Endocrinol., 16: 2657-66 (2002).

Other Studies of Differential Expression in Muscle

The papers collected in this section deal principally with type II diabetes, which is an aging-related disease.

Sreekumar, et al., "Gene expression profile in skeletal muscle of type 2 diabetes and the effect of insulin treatment," *Diabetes* 51: 1913 (June 2002) surveyed 6,451 genes, and identified 85 genes for which there was an alteration in skeletal muscle transcription in diabetic patients after withdrawal of insulin treatment. Subsequent insulin treatment resulted in further changes in transcription of 74 of the 85 genes (15 increased, 59 decreased), and also resulted in alteration of 29 additional gene transcripts.

Mootha, et al., "PCG-1 α responsive genes involved in oxidative phosphorylation are coordinatively downregulated in human diabetes," *Nature Genetics* 34(3); 267 (July 2003), used DNA microarrays to detect changes in the expression of sets of related genes, rather than of individual genes. They classified over 22,000 genes into 149 data sets; some of these data sets overlapped. They looked for a statistical

correlation between the overall rank order of the genes in differential expression, and the groups to which the genes belonged. Expression was compared pairwise among three groups: males with normal glucose tolerance; males with impaired glucose tolerance; and males with type 2 diabetes. The set with the highest enrichment score (the one whose members ranked highly most often relative to chance expectation) was an internally curated set of 106 genes involved in oxidative phosphorylation. While the average decrease for the individual genes was modest (~20%), it was also consistent, being observed in 89% (94/106) of the genes in question. This paper is reviewed by Toye and Gauguier, "Genetics and functional genomics of type 2 diabetes mellitus", *Genome Biology*, 4: 241 (2003).

Patti, et al., "Coordinated reduction of genes of oxidative metabolism in humans with insulin resistance and diabetes: Potential role of PGC1 and NRF1", *Proc. Nat. Acad. Sci. (USA)*, 100(14): 8466 (July 8, 2003) used microarrays to analyze skeletal muscle expression of genes in nondiabetic insulin-resistant subjects at high risk for diabetes (based on family history of diabetes and Mexican-American ethnicity) and diabetic Mexican-American subjects. Of 7,129 sequences represented on the microarray, 187 were differentially expressed between control and diabetic subjects. However, no single gene remained significantly differentially expressed after controlling for multiple comparison false discovery by using the Benjamini-Hochberg method, see Benjamini, et al., *J. R. Stat. Soc. Ser. B.* 57:289-300 (1995); Dudait, et al., *Stat. Sin.* 12: 111-139 (2002). Consequently, Patti et al. sought to identify groups of related genes with similar patterns of differential expression using MAPP FINDER and ONTOEXPRESS. According to MAPP FINDER, the top-ranked cellular component terms were mitochondrion, mitochondrial membrane,

mitochondrial inner membrane, and ribosome, and the top-ranked process term was ATP biosynthesis. According to ONTOEXPRESS, the over-represented groups were energy generation, protein biosynthesis/ribosomal proteins, RNA binding, ribosomal structural protein, and ATP synthase complex.

Huang, Xudong, "Identification of abnormally expressed genes in skeletal muscle contributing to insulin resistance and type 2 diabetes", Thesis, document id: 9576 Lunds University 2002, reported differential expression of the mitochondrially-encoded ND1 gene in human diabetic patients and of the nuclear-encoded cathepsin L gene in mice.

Standaert, et al., "Skeletal muscle insulin resistance in obesity-associated type 2 diabetes in monkeys is linked to a defect in insulin activation of protein kinase C-zeta/lambda/iota Diabetes 51: 2936 (Oct. 2002). the authors concluded that defective activation of atypical PKCs played an important role in the pathogenesis of peripheral insulin resistance in both obese prediabetic and diabetic monkeys. They attributed this linkage to the apparent requirement for aPKCs during insulin-stimulated glucose transport.

Srommer, et al., Am. J. Physiol., "Skeletal muscle insulin resistance after trauma: insulin signaling and glucose transport", 275(2 Pt. 1): E3518(Aug. 1998) concluded that insulin resistance in skeletal muscle after surgical trauma is associated with reduced glucose transport but not with impaired glucose signaling to PI 3-kinase or its downstream target, Akt.

Other Differential/Subtractive Hybridization Studies of Interest

Zhang, et al., Kidney International, 56:549-558 (1999) identified genes up-regulated in 5/6 nephrectomized (subtotal renal ablation) mouse kidney by a PCR-based

subtraction method. Ten known and nine novel genes were identified. The ultimate goal was to identify genes involved in glomerular hyperfiltration and hypertrophy. Melia, et al., *Endocrinol.*, 139:688-95 (1998) applied subtractive hybridization methods for the identification of androgen-regulated genes in mouse kidney. The treatment mice were dosed with dihydrotestosterone, an androgen. Kidney androgen-regulated protein gene was used as a positive control, as it is known to be up-regulated by DHT.

See also Holland, et al., Abstract 607, "Identification of Genes Possibly Involved in Nephropathy of Bovine Growth Hormone Transgenic Mice" (Endocrine Society Meeting, June 22, 2000) and Coschigano, et al., Abstract 333, "Identification of Genes Potentially Involved in Kidney Protection During Diabetes" (Endocrine Society Meeting, June 22, 2000).

The following differential hybridization articles may also be of interest: Wada, et al., "Gene expression profile in streptozotocin-induced diabetic mice kidneys undergoing glomerulosclerosis", *Kidney Int.*, 59:1363-73 (2001); Song, et al., "Cloning of a novel gene in the human kidney homologous to rat munc13S: its potential role in diabetic nephropathy", *Kidney Int.*, 53:1689-95 (1998); Page, et al., "Isolation of diabetes-associated kidney genes using differential display", *Biochem. Biophys. Res. Comm.*, 232:49-53 (1997); Peradi, "Subtractive hybridization claims: An efficient technique to detect overexpressed mRNAs in diabetic nephropathy," *Kidney Int.* 53:926-31 (1998); Condorelli, *EMBO J.*, 17:3858-66 (1998); See also WO00/66784 (differential hybridization screening for brown adipose tissue); PCT/US00/12366, filed May 5, 2000 (differential hybridization screening for liver).

Apoptosis and *CIDE-A*

Apoptosis is a form of programmed cell death that occurs in an active and controlled manner to eliminate unwanted cells. Apoptotic cells undergo an orchestrated cascade of morphological changes such as membrane blebbing, nuclear shrinkage, chromatin condensation, and formation of apoptotic bodies which then undergo phagocytosis by neighboring cells. One of the hallmarks of cellular apoptosis is the cleavage of chromosomal DNA into discrete oligonucleosomal size fragments. This orderly removal of unwanted cells minimizes the release of cellular components that may affect neighboring tissue. In contrast, membrane rupture and release of cellular components during necrosis often leads to tissue inflammation.

The process of apoptosis is highly conserved and involves the activation of the caspase cascade. Cohen, GM. (1997) Caspases: the executioners of apoptosis. *Biochem. J.* 326:1-16; Budihardjo, I., Oliver, H., Lutter, M., Luo, X., Wang, X. (1999) Biochemical pathways of caspase activation during apoptosis. *Annu. Rev. Cell. Dev. Biol.* 15:269-290; Jacobson, M.D., Weil, M., Raff, M.C. (1997) Programmed cell death in animal development. *Cell* 88:347-354. Caspases are a family of serine proteases that are synthesized as inactive proenzymes. Their activation by apoptotic signals such as CD95 (Fas) death receptor activation or tumor necrosis factor results in the cleavage of specific target proteins and execution of the apoptotic program. Apoptosis may occur by either an extrinsic pathway involving the activation of cell surface death receptors (DR) or by an intrinsic mitochondrial pathway. Yoon, J-H. Gores G.J. (2002) Death receptor-mediated apoptosis and the liver. *J. Hepatology* 37:400-410.

These pathways are not mutually exclusive and some cell types require the activation of both pathways for

maximal apoptotic signaling. In type-I cells, death receptor activation leads to the recruitment and activation of caspases-8/10 and the rapid cleavage and activation of caspase-3 in a mitochondrial-independent manner.

Hepatocytes are members of the Type-II cells in which mitochondria are essential for DR-mediated apoptosis. Scaffidi, C., Fulda, S., Srinivasan, A., Friesen, C., Li, F., Tomaselli, K.J., Debatin, K.M., Krammer, P.H., Peter, M.E. (1998) Two CD95 (APO-1/Fas) signaling pathways. *EMBO J.* 17:1675-1687. In this pathway, the pro-apoptotic protein Bid is truncated by activated caspases-8/10 and translocates to the mitochondria. Luo, X., Budihardjo, I., Zou, H., Slaughter, C., Wang, X. (1998) Bid, a Bcl2 interacting protein, mediates cytochrome c release from mitochondria in response to activation of cell surface death receptors. *Cell* 94:481-490; Li, H., Zhu, H., Xu, C.J., Yuan, J. (1998) Cleavage of BID by caspase 8 mediates the mitochondrial damage in the Fas pathway of apoptosis. *Cell* 94:491-501. This translocation leads to mitochondrial cytochrome c release and eventual activation of caspases-3 and 7 via cleavage by activated caspase-9.

One of the substrates for activated caspase-3 is the DNA fragmentation factor (DFF). DFF is composed of a 45 kDa regulatory subunit (DFF45) and a 40 kDa catalytic subunit (DFF40). Liu, X., Zou, H., Slaughter, C., Wang, X. (1997) DFF, a heterodimeric protein that functions downstream of caspase-3 to trigger DNA fragmentation during apoptosis. *Cell* 89:175-184. DFF45 cleavage by activated caspase-3 results in its dissociation from DFF40 and allows the caspase-activated DNase (CAD) activity of DFF40 to cleave chromosomal DNA into oligonucleosomal size fragments. Liu, X., Li, P., Widlak, P., Zou, H., Luo, X., Garrard, W.T., Wang, X. (1998) The 40-kDa subunit of DNA fragmentation factor induces DNA fragmentation and chromatin

condensation during apoptosis. *Proc. Natl. Acad. Sci. USA.* 95:8461-8466; Halenbeck, R., MacDonald, H., Roulston, A., Chen, T.T., Conroy, L., Williams, L.T. (1998) CPAN, a human nuclease regulated by the caspase-sensitive inhibitor DFF45. *Curr Biol.* 8:537-540; Nagata, S. (2000) Apoptotic DNA fragmentation. *Exp. Cell Res.* 256:12-8.

Recently, a novel family of cell-death-inducing DFF45-like effectors (CIDEs) have been identified that includes CIDE-A, CIDE-B and CIDE-3/FSP2. Inohara, N., Koseki, T., Chen, S., Wu, X., Nunez, G. (1998) CIDE, a novel family of cell death activators with homology to the 45 kDa subunit of the DNA fragmentation factor. *EMBO J.* 17:2526-2533; Danesch, U., Hoeck, W., Ringold, G.M. (1992) Cloning and transcriptional regulation of a novel adipocyte-specific gene, FSP27. CAAT-enhancer-binding protein (C/EBP) and C/EBP-like proteins interact with sequences required for differentiation-dependent expression. *J. Biol. Chem.* 267:7185-7193; Liang, L., Zhao, M., Xu, Z., Yokoyama, K.K., Li, T. (2003) Molecular cloning and characterization of CIDE-3, a novel member of the cell-death-inducing DNA-fragmentation-factor (DFF45)-like effector family. *Biochem. J.* 370:195-203.

The CIDEs contain an N-terminal domain that shares homology with the N-terminal region of DFF45 and may represent a regulatory region via protein interaction. See Inohara, supra; Lugovskoy, A.A., Zhou, P., Chou, J.J., McCarty, J.S., Li, P., Wagner, G. (1999) Solution structure of the CIDE-N domain of CIDE-B and a model for CIDE-N/CIDE-N interactions in the DNA fragmentation pathway of apoptosis. *Cell* 9:747-755. The family members also share a C-terminal domain that is necessary and sufficient for inducing cell death and DNA fragmentation; see Inohara supra. The overexpression of CIDE-A induces cell death that can be inhibited by DFF45. However, CIDE-A-induced

apoptosis is not inhibited by caspase-8 inhibitors thereby suggesting the presence of additional, caspase-independent, pathway(s) for the induction of apoptosis, see Inohara supra. Previous reports have indicated that human and mouse CIDE-A are expressed in several tissues such as brown adipose tissue (BAT) and heart and are localized to the mitochondria, Zhou, Z., Yon Toh, S., Chen, Z., Guo, K., Ng, C.P., Ponniah, S., Lin, S.C., Hong, W., Li, P. (2003) Cidea-deficient mice have lean phenotype and are resistant to obesity. Nat. Genet. 35:49-56. . In addition to the ability to induce apoptosis, CIDE-A can interact and inhibit UCP1 in BAT and may therefore play a role in regulating energy balance, see Zhou supra.

Previous reports have indicated that CIDE-A is not expressed in either adult human or mouse liver tissue, see Inohara supra, Zhou supra.

The human protein cell death activator CIDE-A is of particular interest because of its highly dramatic change in liver expression with age, first demonstrated in our Kopchick7 application, supra. CIDE-A expression is elevated in older normal mice. CIDE-A expression was studied for normal C57BI/6J mouse ages 35, 49, 77, 133, 207, 403 and 558 days. Expression is low at the first five data points, then rises sharply at 403 days, and again at 558 days.

CIDE-A was therefore classified as an "unfavorable protein", i.e., it was taught that an antagonist to CIDE-A could retard biological aging.

In Kopchick7A-PCT we reported that CIDE-A is also prematurely expressed in hyperinsulinemic and type-II diabetic mouse liver tissue. CIDE-A expression also correlates with liver steatosis in diet-induced obesity, hyperinsulinemia and type-II diabetes. These observations suggest an additional pathway of apoptotic cell death in

Non-Alcoholic Fatty Liver Disease (NAFLD) and that CIDE-A may play a role in this serious disease and potentially in liver dysfunction associated with type-II diabetes.

SUMMARY OF THE INVENTION

Our attention recently has focused on the generation of muscle mRNA expression profiles and the identification of genes involved in the aging process. We have therefore explored the genetic changes in the muscle of C57Bl/6 mice that occur during the ageing process, observing the gene expression patterns at many different time points.

Nucleic acid hybridization techniques on gene chips have been used to identify mouse genes that are differentially expressed in mice, depending upon their age. We have utilized the Amersham product code: 300013 Codelink UniSet Mouse I Bioarray to determine the level of gene expression of approximately 10,000 mouse genes in the muscle of mice with average ages of 35, 49, 77, 118, 133, 207, 403, 558 and 725 days.

In essence, complementary RNA derived from mice of different ages was screened for hybridization with oligonucleotide probes each specific to a particular mouse database DNA, the latter being identified, by database accession number, by the gene manufacturer. Each database DNA in turn was also identified by the gene chip manufacturer as representative of a particular mouse gene cluster (Unigene).

In most cases, this database DNA sequence is a full length genomic DNA or cDNA sequence, and is therefore either identical to, or otherwise encodes the same protein as does, a natural full-length genomic DNA protein coding sequence. Those which don't present at least a partial sequence of a natural gene or its cDNA equivalent.

For the sake of simplicity, all of these mouse database DNA sequences, whether full-length or partial, and whether cDNA or genomic DNA, are referred to herein as "mouse genes". When only the genomic sequence is intended, we will refer specifically to "genomic DNA" or "gDNA".

The sequences in the protein databases are determined either by directly sequencing the protein or, more commonly, by sequencing a DNA, and then determining the translated amino acid sequence in accordance with the Genetic Code. All of the mouse sequences in the mouse polypeptide database are referred to herein as "mouse proteins" regardless of whether they are in fact full length sequences.

Mouse genes which were differentially expressed (younger vs. older), as measured by different levels of hybridization of the respective cRNA samples with the particular probe corresponding to that mouse gene, were identified.

Favorable behavior is when expression decreases with age. Substantially favorable behavior is when the ratio of younger value to older value is at least two fold. Unfavorable behavior is when expression increases with age. Substantially unfavorable behavior is when the ratio of older value to younger value is at least two fold.

A mouse gene is considered to be "favorable" (more precisely, "wholly favorable") for the purpose of Master Table 1 (especially subtable 1A) if, for at least one of the time comparisons set forth in the Examples, it exhibited substantially favorable behavior, and if, for all the other comparisons, it at least did not exhibit substantially unfavorable behavior. Note that the classification of a gene as favorable for purpose of the Master Table does not mean that it must have exhibited substantially favorable behavior for all of the comparisons set forth in the Examples.

A mouse gene is considered to be "unfavorable" (more precisely, "wholly unfavorable") for the purpose of the Master Table 1 (especially subtable 1B) if, for at least one of the time comparisons set forth in the Examples, it

exhibited substantially unfavorable behavior, and if, for all the other comparisons, it at least did not exhibit substantially favorable behavior.

A mouse gene is considered to be "mixed" (i.e., partially favorable and partially unfavorable) for the purpose of the Master Table, especially subtable 1C, if for at least one of the time comparisons set forth in the Examples it exhibited substantially favorable behavior and if for at least one of the other such comparisons it exhibited substantially unfavorable behavior.

The expression of a gene may first rise, then fall, with increasing age. Or it may first fall, and then rise. These are just the two simplest of several possible "mixed" expression patterns.

Thus, we can subdivide the "favorables" into wholly and partially favorables. Likewise, we can subdivide the unfavorables into wholly and partially unfavorables. The genes/proteins with "mixed" expression patterns are, by definition, both partially favorable and partially unfavorable. In general, use of the wholly favorable or wholly unfavorable genes/proteins is preferred to use of the partially favorable or partially unfavorable ones.

It is evident from the foregoing that mixed genes/proteins are those exhibiting a combination of favorable and unfavorable behavior. A mixed gene/protein can be used as would a favorable gene/protein if its favorable behavior outweighs the unfavorable. It can be used as would an unfavorable gene/protein if its unfavorable behavior outweighs the favorable. Preferably, they are used in conjunction with other agents that affect their balance of favorable and unfavorable behavior. Use of mixed genes/proteins is, in general, less desirable than use of purely favorable or purely unfavorable genes/proteins.

It will be appreciated that the comparisons set forth in the Examples are not exhaustive and that it is possible that a mouse gene which, on the basis of those comparisons, is classified as a "favorable" gene in the Master Table) may turn out, if additional time points are considered, to sometimes exhibit substantially unfavorable behavior. Nonetheless, such a gene will still be considered a "favorable" gene for the purpose of the Master Table and the claims referring to the Master Table. Likewise, a gene which, on the basis of those comparisons, was classified as an "unfavorable" gene in the Master Table may prove, under more detailed examination, to sometimes exhibit substantially favorable behavior. Nonetheless, it will retain "unfavorable" classification for the purpose of the Master Table and the claims referring thereto.

The "favorable", "unfavorable" and "mixed" mouse proteins are thus those listed in the Master Table as encoded by the listed "favorable", "unfavorable" and "mixed" mouse genes, respectively, or which otherwise correspond to those mouse genes.

Related human genes (database DNAs) and proteins were identified by searching a database comprising human DNAs or proteins for sequences corresponding to (i.e., homologous to, i.e., which could be aligned in a statistically significant manner to) the mouse gene or protein. More than one human protein may be identified as corresponding to a particular mouse chip probe and to a particular mouse gene.

Note that the terms "human genes" and "human proteins" are used in a manner analogous to that already discussed in the case of "mouse genes" and "mouse proteins".

As used herein, the term "corresponding" does not mean identical, but rather implies the existence of a statistically significant sequence similarity, such as one

sufficient to qualify the human protein or gene as a homologous protein or DNA as defined below. The greater the degree of relationship as thus defined (i.e., by the statistical significance of each alignment used to connect the mouse chip DNA, and the corresponding mouse gene/cDNA, to the human protein or gene, measured by an E value), the more close the correspondence. The connection may be direct (mouse gene/cDNA to human protein) or indirect (e.g., mouse gene/cDNA to human gene, human gene to human protein).

In general, the human genes/proteins which most closely correspond, directly or indirectly, to the mouse gene/cDNA are preferred, such as the one(s) with the highest, top two highest, top three highest, top four highest, top five highest, and top ten highest E values for the final alignment in the connection process. The human genes/proteins deemed to correspond to our mouse genes are identified in the Master Tables.

Note that it is possible to identify homologous full-length human genes and proteins, if they are present in the database, even if the query mouse DNA or protein sequence is not a full-length sequence.

If there is no homologous full-length human gene or protein in the database, but there is a partial one, the latter may nonetheless be useful. For example, a partial protein may still have biological activity, and a molecule which binds the partial protein may also bind the full-length protein so as to antagonize a biological activity of the full-length protein. Likewise, a partial human gene may encode a partial protein which has biological activity, or the gene may be useful in the design of a hybridization probe or in the design of a therapeutic antisense DNA.

The partial genes and protein sequences may of course also be used in the design of probes intended to identify the full length gene or protein sequence.

Agents which bind the "favorable" and "unfavorable" nucleic acids (e.g., the agent is a substantially complementary nucleic acid hybridization probe), or the corresponding proteins (e.g., an antibody vs. the protein) may be used to estimate the biological age of a human subject, or to predict the rate of biological aging in a human subject (i.e, to evaluate whether a human subject is at increased or decreased risk for faster-than-normal biological aging). A subject with one or more elevated "unfavorable" and/or one or more depressed "favorable" genes/proteins is at increased risk, and one with one or more elevated "favorable" and/or one or more depressed "unfavorable" genes/proteins is at decreased risk.

The assay may be used as a preliminary screening assay to select subjects for further analysis, or as a formal diagnostic assay.

The identification of the related genes and proteins may also be useful in protecting humans against faster-than-normal or even normal aging (hereinafter, "the disorders"). They may be used to reduce a rate of biological aging in the subject, and/or delay the time of onset, or reduce the severity, of an undesirable age-related phenotype in said subject, and/or protect against an age-related disease.

Thus, Applicants contemplate:

(1) use of the "favorable" mouse DNAs (or fragments thereof) of the Master Tables (below) to isolate or identify related human DNAs;

(2) use of human DNAs, related to favorable mouse DNAs, to express the corresponding human proteins;

(3) use of the corresponding human proteins (and mouse proteins, if biologically active in humans), to protect against the disorder(s);

(4) use of the corresponding mouse or human proteins, or nucleic acid probes derived from the mouse or human cDNAs or genes, in diagnostic agents, in assays to measure or predict biological aging or the rate thereof; and

(5) use of the corresponding human or mouse genes or cDNAs therapeutically in gene therapy, to protect against the disorder(s).

Moreover Applicants contemplate:

(1) use of the "unfavorable" mouse DNAs (or fragments thereof) of the Master Tables to isolate or identify related human DNAs;

(2) use of the complement to the "unfavorable" mouse DNAs or related human DNAs, as antisense molecules to inhibit expression of the related human DNAs;

(3) use of the mouse or human DNAs to express the corresponding mouse or human proteins;

(4) use of the corresponding mouse or human proteins, in diagnostic agents, to measure biological aging or the rate thereof;

(5) use of the corresponding mouse or human proteins in assays to determine whether a substance binds to (and hence may neutralize) the protein; and

(6) use of the neutralizing substance to protect against the disorder(s).

Thus, DNAs of interest include those which specifically hybridize to the aforementioned mouse or human genes, and are thus of interest as hybridization assay reagents or for antisense therapy. They also include synthetic DNA sequences

which encode the same polypeptide as is encoded by the database DNA, and thus are useful for producing the polypeptide in cell culture or in situ (i.e., gene therapy). Moreover, they include DNA sequences which encode polypeptides which are substantially structurally identical or conservatively identical in amino acid sequence to the mouse and human proteins identified in the Master Table 1, subtables 1A or 1C. Finally, they include DNA sequences which encode peptide (including antibody) antagonists of the proteins of Master Table 1, subtables 1B or 1C.

Related human DNAs also may be identified by screening human cDNA or genomic DNA libraries using the mouse gene of the Master Table, or a fragment thereof, as a probe.

If the mouse gene of Master Table 1 is not full-length, and there is no closely corresponding full-length mouse gene in the sequence databank, then the mouse DNA may first be used as a hybridization probe to screen a mouse cDNA library to isolate the corresponding full-length sequence. Alternatively, the mouse DNA may be used as a probe to screen a mouse genomic DNA library.

The agents of the present invention may be used alone or in conjunction with each other and/or known anti-aging or anti-age-related disease agents. It is of particular interest to use the agents of the present invention in conjunction with an agent disclosed in one of the related applications cited above, in particular, an antagonist to CIDE-A, the latter having been taught in Kopchick7.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS OF THE INVENTION

Full-Length vs. Partial Length Genes/Proteins

A "full length" gene is here defined as (1) a naturally occurring DNA sequence which begins with an initiation codon (almost always the Met codon, ATG), and ends with a stop codon in phase with said initiation codon (when introns, if any, are ignored), and thereby encodes a naturally occurring polypeptide with biological activity, or a naturally occurring precursor thereof, or (2) a synthetic DNA sequence which encodes the same polypeptide as that which is encoded by (1). The gene may, but need not, include introns.

A "full-length" protein is here defined as a naturally occurring protein encoded by a full-length gene, or a protein derived naturally by post-translational modification of such a protein. Thus, it includes mature proteins, proproteins, preproteins and preproproteins. It also includes substitution and extension mutants of such naturally occurring proteins.

Anatomy and Physiology of Muscle

Muscle tissue constitutes about 40% of the body mass. Muscles may be classified by location, i.e., skeletal if attached to bone, cardiac if forming the wall of the heart, and visceral if associated with another body organ. Muscles may also be classified as voluntary or involuntary, depending on how their contractions and relaxations are controlled. Skeletal muscles are voluntary, while cardiac and visceral muscles are involuntary. It is also possible to classify muscles morphologically; skeletal and cardiac muscle cells are striated, whereas visceral muscle cells are not.

Each skeletal muscle is composed of many individual muscle cells called muscle fibers. The fibers are held together by fibrous connective-tissue membranes called fascia. The fascium which envelops the entire muscle is the epimysium, and the fascia which penetrate the muscle, separating the fibers into bundles (fasciculi) are called perimysium. Very thin fascia (endomysium) sheath each muscle fiber. Skeletal muscles are attached either directly to a bone, or indirectly through a tendon.

The individual muscle fibers (cells) comprise threadlike protein structures called myofibrils.

There are over 600 muscles in the human body. We will have occasion later to refer to the gastrocnemius. It is a superficial muscle in the posterior compartment of the lower leg, which together with the underlying soleus forms the characteristic bulge of the calf.

Subjects

For mice, infancy is defined as the period 0 to 21 days after birth. Sexual maturity is reached, on average, at 42 days after birth. The average lifespan is 832 days.

In humans, infancy is defined as the period between birth and two years of age. Sexual maturity in males can occur between 9 and 14 years of age while the average age at first menstrual period for females is 12.6 years. The average human lifespan is 73 years for males and 79 years for females. The maximum verified human lifespan was 122 years, five months and 14 days.

Chronological and Biological Aging

"Aging" is a process of gradual and spontaneous change, resulting in maturation through childhood, puberty, and young adulthood and then primarily a decline in function through middle and late age. Aging thus has both the

positive component of development/maturation and the negative component of decline.

"Senescence" refers strictly to the undesirable changes that occur as a result of post-maturation aging. Some of the changes which occur in post-maturation aging are not deleterious to health (e.g., gray hair, baldness), and some may even be desirable (e.g., increased wisdom and experience). In contrast, the memory impairment that occurs with age is considered senescence. However, we will hereafter use "aging" per se to refer to "senescence", and use "maturation" to refer to pre-maturation development.

There is increased mortality with age after maturation. There is also a progressive decrease in physiological capacity with age; but the rate of physiological decline varies from organ to organ and from individual to individual. The physiological decline results in a reduced ability to respond adaptively to environmental stimuli, and increased susceptibility and vulnerability to disease.

"Aging is the accumulation of diverse adverse changes that increase the risk of death. These changes can be attributed to development, genetic defects, the environment, disease, and the inborn aging process. The chance of death at a given age serves as a measure of the number of accumulated changes, that is, of physiologic age, and the rate of change of this measure, as the rate of aging."

Harman, Ann. N.Y. Acad. Sci. 854:1-7 (1998).

Preferably, the agents of the present invention inhibit aging for at least a subpopulation of mature (post-puberty) adult subjects.

The term "healthy aging" (sometimes called "successful aging") refers to post-maturation changes in the body that occur with increasing age even in the absence of an overt disease. However, increased age is a risk factor for many diseases ("age-related diseases"), and hence "total aging"

includes both the basal effects of healthy aging and the effects of any age-related disease. (Most literature uses the term "normal aging" as a synonym for "healthy aging", but a minority use it to refer to "total aging". To minimize confusion, we will try to avoid the term "normal aging", but if we use it, it is as a synonym for "healthy aging".) Some scientists have suggested that normal aging changes should be defined as those which are universal, degenerative, progressive and intrinsic.

Preferably, the agents of the present invention inhibit healthy aging for at least a subpopulation of mature (post-puberty) adult subjects.

In both aging and senescence, many physiologic functions decline, but normal decline is not usually considered the same as disease. The distinction between normal decline and disease is often but not always clear and may be due only to statistical distribution. Glucose intolerance is considered consistent with healthy aging, but diabetes is considered a disease, although a very common one. Cognitive decline is nearly universal with advanced age and is considered healthy aging; however, cognitive decline consistent with dementia, although common in late life, is considered a disease (as in the case of Alzheimer's, a conclusion supported by analysis of brain tissue at autopsy). A decline in maximal heart rate is typical of healthy aging. In contrast, coronary heart disease is an age-related disease. A decline in bone density is considered healthy aging, but when it drops to 2.5 SD below the young adult mean, it is called osteoporosis. Generally speaking, the changes typical of healthy aging are gradual, while those typical of a disorder can be rapid.

The term average (median) "lifespan" is the chronological age to which 50% of a given population survive. The maximum lifespan potential is the maximum age achievable by a member of the population. As a practical matter, it is estimated as the age reached by the longest lived member (or former member) of the population. The (average) life expectancy is the number of remaining years that an individual of a given age can expect to live, based on the average remaining lifespans of a group of matched individuals.

The most widely accepted method of measuring the rate of aging is by reference to the average or the maximum lifespan. If a drug treatment achieves a statistically significant improvement in average or maximum lifespan in the treatment group over the control group, then it is inferred that the rate of aging was retarded in the treatment group. Similarly, one can compare long-term survival between the two groups.

Preferably, the agents of the present invention have the effect of increasing the average lifespan and/or the maximum lifespan for at least a subpopulation of mature (post-puberty) adult subjects. This subpopulation may be defined by sex and/or age. If defined in part by age, then it may be defined by a minimum age (e.g., at least 30, at least 40, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 90, etc.) or by a maximum age (not more than 40, not more than 50, not more than 55, not more than 60, not more than 65, not more than 70, not more than 75, not more than 80, not more than 90, not more than 100, etc.), or by a rational combination of a minimum age and a maximum age so as to define a preferred close-ended age range, e.g., 55-75.

The subpopulation may additionally be defined by race, e.g., caucasian, negroid or oriental, and/or by ethnic

group, and/or by place of residence (e.g., North America, Europe).

The subpopulation may additionally be defined by non-age risk factors for age-associated diseases, e.g., by blood pressure, body mass index, etc.

Preferably, the subpopulation in which an agent of the present invention is reasonably expected to be effective is large, e.g., in the United States, preferably at least 100,000 individuals, more preferably at least 1,000,000 individuals, still more preferably at least 10,000,000, even more preferably at least 20,000,000, most preferably at least 40,000,000.

By way of comparison, according to the 2000 U.S. Census, the U.S. population, by age, was

Age	Pop (mil)
15-19	20.2
20-24	19.0
25-29	19.4
30-34	20.5
35-39	22.7
40-44	22.4
45-49	20.1
50-54	17.6
55-59	13.5
60-64	10.8
65-69	9.5
70-74	8.9
75-79	7.4
80-84	4.9
85+	4.2

For any given chronological age, statisticians can define the probability of living to a particular later age. These expectancies can be calculated for the entire age cohort, or broken down by sex, race, country of residence, etc. Individuals who live longer than expected can be said, after the fact, to have biologically aged more slowly than their peers. One definition of biological age is that it is a measure of one's position in one's life span, i.e., $\text{biological age} = \text{position in own life span (as fraction in range 0..1)} \times \text{average life span for species}$. This simple definition carries with it the implicit assumption that the rate of biological aging is constant. It also has the practical problem of determining one's own life span before death. We will present a more practical definition shortly.

The problem with lifespan studies is that they are extremely time-consuming. A maximum lifespan study in mice can take 4-5 years. A maximum lifespan study in dogs or cats would take 15-20 years, in monkeys, 30-40 years, and in humans, over 100 years. Even if the human study group were of sexagenarians, it would take 40-60 years to complete the study.

Hence, scientists have sought to identify biological markers (biomarkers) of biological aging, that is, characteristics that can be measured while the subjects are still alive, which correlate to lifespan. These biological markers can be used to calculate a "biological age" (syn. "Physiological age"); it is the chronological age at which an average member of the population (or relevant subpopulation) would have the same value of a biomarker of biological aging (or the same value of a composite measure of biomarkers of biological aging) as does the subject. This is the definition that will be used in this disclosure, unless otherwise stated.

The effect of aging varies from system to system, organ to organ, etc. For example, between ages 30 and 70 years, nerve conduction velocity decreases by only about 10%, but renal function decreases on average by nearly 40%. Thus, there isn't just one biological age for a subject. By a suitable choice of biomarker, one may obtain a whole organism, or a system-, organ- or tissue-specific measure of biological aging, e.g., one can say that a person has the nervous system of a 30 year old but the renal system of a 60 year old. Biomarkers may measure changes at the molecular, cellular, tissue, organ, system or whole organism levels.

Generally speaking, in the absence of some form of intervention (drugs, diet, exercise, etc.), biological ages will increase with time. The agents of the present invention preferably reduce the time rate of change of a biological age of the subject. The term "a biological age" could refer to the overall biological age of the subject, to the biological age of a particular system, organ or tissue of that subject, or to some combination of the foregoing. More preferably, the agents of the present invention cannot only reduce the rate of increase of a biological age of the subject, but can actually reduce a biological age of the subject.

A simple biologic marker (biomarker) is a single biochemical, cellular, structural or functional indicator of an event in a biologic system or sample. A composite biomarker is a mathematical combination of two or more simple biomarkers. (Chronological age may be one of the components of a composite biomarker.)

A plausible biomarker of biological age would be a biomarker which shows a cross-sectional and/or longitudinal correlation with chronological age. Nakamura suggests that it is desirable that a biomarker show (a) significant cross-

sectional correlation with chronological age, (b) significant longitudinal change in the same direction as the cross-sectional correlation, (c) significant stability of individual differences, and (d) rate of age-related change proportional to differences in life span among related species. Cp. Nakamura, *Exp Gerontol.* 29(2):151-77 (1994), using desiderata (a)-(c). A superior biomarker of biological age would be a better predictor of lifespan than is chronological age (preferably for a chronological age at which 90% of the population is still alive).

The biomarker preferably also satisfies one or more of the following desiderata: a statistically significant age-related change is apparent in humans after a period of at most a few years; not affected dramatically by physical conditioning (e.g., exercise), diet, and drug therapy (unless it is possible to discount these confounding influences, e.g., by reference to a second marker which measures them); can be tested repeatedly without harming the subject; works in lab animals as well as humans; simple and inexpensive to use; does not alter the result of subsequent tests for other biomarkers if it is to be used in conjunction with them; monitors a basic process that underlies the aging process, not the effects of disease.

Preferably, if the biomarker works in lab animals, there is a statistically significant difference in the value of the biomarker between groups of food-restricted and normally-fed animals. It has been shown in some mammalian species that dietary restriction without malnutrition (e.g., caloric decrease of up to 40% from ad libitum feeding) increases lifespan.

A biomarker of aging may be used to predict, instead of lifespan, the "Healthy Active Life Expectancy" (HALE) or the "Quality Adjusted Life Years" (QALY), or a similar measure which takes into account the quality of life before death as

well as the time of death itself. For HALE, see Jagger, in *Outcomes Assessment for Healthcare in Elderly People*, 67-76 (Farrand Press: 1997). For QALY, see Rosser RM. A health index and output measure, in Stewart SR and Rosser RM (eds) *Quality of Life: Assessment and Application*. Lancaster: MTP, 1988.

A biomarker of aging may be used to predict, instead of lifespan, the timing and/or severity of a change in one or more age-related phenotypes as described below.

A biomarker of aging may be used to estimate, rather than overall biological age for a subject, a biological age for a specific body system or organ. The determination of the biological age of the muscle, and the inhibition of biological aging of the muscle, are of particular interest.

Body systems include the nervous system (including the brain, the sensory organs, and the sense receptors of the skin), the cardiovascular system (includes the heart, the red blood cells and the reticuloendothelial system), the respiratory system, the gastrointestinal system, the endocrine system (pituitary, thyroid, parathyroid and adrenal glands, gonads, pancreas, and paraganglia), the musculoskeletal system, the urinary system (kidneys, bladder, ureters, urethra), the reproductive system and the immune system (bone marrow, thymus, lymph nodes, spleen, lymphoid tissue, white blood cells, and immunoglobulins). A biomarker may be useful in estimating the biological age of a system because the biomarker is a chemical produced by that system, because it is a chemical whose activity is primarily exerted within that system, because it is indicative of the morphological character or functional activity of that system, etc. A given biomarker may be thus associated with more than one system. In a like manner, a biomarker may be associated with the biological age, and hence the state, of a particular organ or tissue.

The prediction of lifespan, or of duration of system or organ function at or above a particular desired level, may require knowledge of the value of at least one biomarker of aging at two or more times, adequately spaced, rather than of the value at a single time. See McClearn, Biomarkers of Age and Aging, *Exp. Gerontol.*, 32:87-94 (1997).

The levels (or changes in levels) of the human proteins identified in this specification, and their corresponding mRNAs, may be used as simple biomarkers (direct or inverse) of biological aging. They may be used in conjunction with each other, or other simple biomarkers, in a composite biomarker.

Once several plausible simple biomarkers have been identified, a composite biomarker may be obtained by standard mathematical techniques, such as multiple regression, principal component analysis, cluster analysis, neural net analysis, and so forth. As a preliminary to such analysis, the values may be standardized, e.g., by converting the raw scores into z-scores based on the distributions for each simple biomarker.

For example, principal component analysis can be used to analyze the variation of lifespan with different observables, and the factor score coefficients from the first principal component can be used to derive an equation for estimating a biological age score. Nakamura, *Exp Gerontol.* 29(2):151-77 (1994). This approach was used to obtain the following BAS (for healthy Japanese women aged 28-80): $BAS = -4.37 - 0.998FEV_{1.0} + 0.022SBP + 0.133MCH + 0.018GLU - 1.505 A/G \text{ RATIO}$, where $FEV_{1.0}$ is the forced expiratory volume in 1 sec. (Liters), SBP is the systolic blood pressure (mm Hg), MCH is the mean corpuscular hemoglobin (pg), GLU is glucose (mg/dl), and A/G RATIO is the ratio of albumin to globulin. The relative importance of these five biomarkers was 33.7%, 25.1%, 17.1%, 14.8% and 8.9%,

respectively. Ueno, et al., ⁴¹ "Biomarkers of Aging in Women and the Rate of Longitudinal Changes," J. Physiol. Anthropol. 22(1): 37-46 (Jan. 2003).

It should be noted that particularly when evaluating the overall biological age of the subject, it is not necessarily most desirable to weight all systems or all organs equally. One may find it more desirable to give greater weight to the system or organ with the highest biological age in calculating the overall biological age, because it is presumably more likely to deteriorate or fail, resulting in death. Appropriate statistical analysis can be used to find the weighting scheme resulting in the best prediction of lifespan.

In the H-SCAN (Hoch Company) test, a composite of 12 simple biomarkers is used to measure human aging:

SENSORY

1. Highest audible pitch (kHz)
2. Visual accommodation (diopters)
3. Vibrotactile sensitivity (dB)

MOTOR

4. Muscle Movement time (sec)
5. Muscle Movement time with decision (sec)
6. Alternate button tapping time (sec)

COGNITIVE

7. Memory, length of sequence
8. Auditory reaction time (sec)
9. Visual reaction time (sec)
10. Visual Reaction time with decision (sec)

PULMONARY

11. Forced vital capacity (liters)
12. Forced expiratory Volume- 1 sec (liters)

See Hochschild, R., Journal of Gerontology [Biological Science] 45(6):B187-214; 1990).

According to a website discussing the H-SCAN test, "Biomarkers of aging are characteristics of an organism that correlate in large groups with chronological age and mortality. Of particular value in human applications are biomarkers of aging that also correlate with the quality of life in later life in the sense that they involve functions that are crucial to carrying out the activities of daily living.... A single biomarker of aging is limited by the fact that it measures only one isolated characteristic and is hardly representative of the diversity of functional and structural concomitants of aging.... Biological age, in contrast to chronological age, is an individual's hypothetical age calculated from scores obtained on a battery of tests of biomarkers of aging. As a first step in the calculation, the age of which each biomarker score is

typical is determined by comparison with scores obtained by a large representative group of persons (or organisms) spanning a range of ages. Then one of a variety of averaging techniques is employed (optionally with standardization steps) to obtain a single index of age, as described in detail by Hochschild. This index varies with, and therefore must be expressed with reference to, the measured biomarkers and the mathematical method of combining scores."

<http://www.longevityinstituteone.com/>

Abbo, USP 6,547,729 teaches determining the biological age (he calls it "performance age") of a subject by (1) for a sample population, determining a regression curve relating some set of observed values for an "indicator" of the functionality of a bodily system to the chronological age of the observed individuals, (2) solving the regression equation to obtain a predicted performance age, given the value of the indicator for the subject. The regression can be based on more than one indicator, i.e., it can be a multiple regression. The sample population can be defined by sex, age range, ethnic composition, and geographic location. The bodily system may be a molecular, cellular, tissue or organ system. The following indicators are suggested by Abbo: nervous system (memory tests, reaction time, serial key tapping, digit recall test, letter fluency, category fluency, nerve conduction velocity), arteries (pulse wave velocity; ankle-brachial index), skeletal system (bone mineral density); lungs (forced vital capacity), heart (ejection fraction; length of time completed on a treadmill stress test), kidneys (creatinine clearance), proteins (glycosylation of hemoglobin), endocrine glands (load level of bioactive testosterone; level of dehydroepiandrosterone sulfate, ratio of urinary 17-ketosteroids/17-hydroxycorticosteroids; growth hormone; IGF-1).

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Preferably, the agents of the invention have a favorable effect on the value of at least one simple biomarker of biological aging, such as any of the plausible biomarkers mentioned anywhere in this specification, other than the level of one of the proteins of the present invention. More preferably, they have a favorable effect on the value of at least two such simple biomarkers of biological aging. Even more preferably, at least one such pair is of markers which are substantially non-correlated ($R^2 < 0.5$) .

Desirably, if more than one simple biomarker is favorably affected, the biomarkers in question reflect different levels of organization, and/or different body components at the same level of organization. For example, a visual reaction time with decision test is on the whole organism level, while a measurement of telomere length is on the cellular level.

A biomarker may, but need not, be an indicator related to one of the postulated causes or contributing factors of aging. It may, but need not, be an indicator of the acute health of a particular body system or organ.

A biomarker may measure behavior, cognitive or sensory function, or motor activity, or some combination thereof. It may measure the level of a type of cell (e.g., a T cell subset, such as CD4, CD4 memory, CD4 naive, and CD4 cells expressing P-glycoprotein) or of a particular molecule (e.g., growth hormone, IGF-1, insulin, DHEAS, an elongation factor, melatonin) or family of structurally or functionally related molecules in a particular body fluid (especially blood) or tissue. For example, lower serum IGF-1 levels are correlated with increasing age, and IGF-1 is produced by

many different tissues. On the other hand, growth hormone is produced by the pituitary gland.

A biomarker may measure an indicator of stress (particularly oxidative stress) and resistance thereto. It has been theorized that free radicals damage biomolecules, leading to aging.

A biomarker may measure protein glycation or other protein modification (e.g., collagen crosslinking). It has been theorized that such modifications contribute to aging.

The biomarker may measure changes in the lengths of telomeres or in the rate of cell division. It has been theorized that telomere shortening beyond a critical length leads the cell to stop proliferating. Average telomere length therefore provides a biomarker as to how many divisions the cell as previously undergone and how many divisions the cell can undergo in the future.

Suggested biomarkers have also included resting heart rate, resting blood pressure, exercise heart rate, percent body fat, flexibility, grip strength, push strength, abdominal strength, body temperature, and skin temperature.

The present invention does not require that all of the biomarkers identified above be validated as indicative of biological age, or that they be equally useful as measures of biological age.

There is an overlap between biomarkers of aging and indicators of functional status. An indicator of functional status is an indicator that defines a functional ability (e.g., physiological, cognitive or physical function). An indicator of functional status may also be related to the increase in morbidity and mortality with chronological age. Such indicators preferably predict physiological, cognitive and physical function in an age-coherent way, and do so

better than chronological age. Preferably, they can predict the years of remaining functionality, and the trajectory toward organ-specific illness in the individual. Also, they are preferably minimally invasive.

Suggested indicators include anthropometric data (body mass index, body composition, bone density, etc.), functional challenge tests (glucose tolerance, forced vital capacity), physiological tests (cholesterol/HDL, glycosylated hemoglobin, homocysteine, etc.) and proteomic tests.

A number of mouse models for human aging exist. See Troen, *supra*, Table 3. The drugs identified by the present invention may be further screened in one or more of these models.

Age-Related Phenotype

An age-related phenotype is an observable change which occurs with age. An age-related phenotype may, but need not, also be a biomarker of biological aging.

Preferably, the agent of the present invention favorably affects at least one age-related phenotype. More preferably, it favorably affects at least two age-related phenotypes, more preferably phenotypes of at least two different body systems.

The age-related phenotype may be a system level phenotype, such as a measure of the condition of the nervous system, respiratory system, immune system, circulatory system, endocrine system, reproductive system, gastrointestinal system, or musculoskeletal system.

The age-related phenotype may be an organ level phenotype, such as a measure of the condition of the brain, eyes, ears, lungs, spleen, heart, pancreas, liver, ovaries, testicles, thyroid, prostate, stomach, intestines, or kidney.

The age-related phenotype may be a tissue level phenotype, such as a measure of the condition of the muscle, skin, connective tissue, nerves, or bones.

The age-related phenotype may be a cellular level phenotype, such as a measure of the condition of the cell wall, mitochondria or chromosomes.

The age-related phenotype may be a molecular level phenotype, such as a measure of the condition of nucleic acids, lipids, proteins, oxidants, and anti-oxidants.

The age-related phenotype may be manifested in a biological fluid, such as blood, urine, saliva, lymphatic fluid or cerebrospinal fluid. The biochemical composition of these fluid may be an overall, system level, organ level, tissue level, etc. phenotype, depending on the specific biochemical and fluid involved.

PHYSIOLOGICAL AGING OF THE HUMAN BODY BY SYSTEMS

SKIN, HAIR, NAILS	Loss of subcutaneous fat, Thinning of skin, Decreased collagen, Nails brittle and flake, Mucous membranes drier, Less sweat glands, Temperature regulation difficult, Hair pigment decreases, Hair thins. Eyelids baggy and wrinkled.
EYES AND VISION	Eyes deeper in sockets; Conjunctiva thinner and yellow; Quantity of tears decreases; Iris fades; Pupils smaller, let in less light; Night and depth vision less; "Floaters" can appear Lens enlarges; Lens becomes less

	transparent, can actually become clouded, results in cataracts; Accommodation decreases, results in presbyopia; Impaired color vision, also - especially greens and blues-- because cones degenerate; Predisposed to glaucoma (Increased pressure in eye, decreased absorption of intraocular fluid; can result in blindness); Macular degeneration becoming more frequent (This is the patch of retina where lens focuses light, Ultimately results in blindness)
EARS AND HEARING LOSS	Irreversible, sensorineural loss (presbycusis) with age (Men more affected than women, Loss occurs in higher range of sound, By 60 years, most adults have trouble hearing above 4000Hz, Normal speech 500-2000Hz)
RESPIRATORY SYSTEM	Lungs become more rigid, Pulmonary function decreases, Number and size of alveoli decreases, Vital capacity declines, Reduction in respiratory fluid, Bony changes in chest cavity
CARDIOVASCULAR SYSTEM	Heart smaller and less elastic with age, By age 70 cardiac output reduced 70%, Heart valves become sclerotic, Heart muscle more irritable, More arrhythmias, Arteries more rigid, Veins dilate
GASTROINTESTINAL SYSTEM	Reduced GI secretions, Reduced GI motility, Decreased weight of liver, Reduced regenerative capacity of liver, Liver metabolizes less efficiently
RENAL SYSTEM	After 40 renal function decreases, By 90 lose 50% of function, Filtration and reabsorption reduced, Size and number of nephrons decrease, Bladder muscles weaken, Less able to clear drugs from system, Smaller kidneys and bladder
REPRODUCTIVE SYSTEM (MALE)	Reduced testosterone level, Testes atrophy and soften, Decrease in sperm production, Seminal fluid decreases and more viscous, Erections take more time, Refractory period after ejaculation may lengthen to days
REPRODUCTIVE SYSTEM (FEMALE)	Declining estrogen and progesterone levels, Ovulation ceases, Introitus constricts and loses elasticity, Vagina atrophies - shorter

	and drier, Uterus shrinks, Breasts pendulous and lose elasticity
NEUROLOGICAL SYSTEM	Neurons of central and peripheral nervous system degenerate, Nerve transmission slows, Hypothalamus less effective in regulating body temperature, Reduced REM sleep, decreased deep sleep, After age 50, lose 1% of neurons each year
MUSCULOSCELETAL SYSTEM	Adipose tissue increases with age, Lean body mass decreases, Bone mineral content diminished, Decrease in height from narrow vertebral spaces, Less resilient connective tissue, Synovial fluid more viscous, May have exaggerated curvature of spine
IMMUNE SYSTEM	Decline in immune function, Trouble differentiating between self and non-self - more auto-immune problems, Decreases antibody response, Fatty marrow replaced red marrow, Vitamin B12 absorption might decrease - decreased hemoglobin and hematocrit
ENDOCRINE SYSTEM	Decreased ability to tolerate stress - best seen in glucose metabolism, Estrogen levels decrease in women, Other hormonal decreases include testosterone, aldosterone, cortisol, progesterone

Adapted from http://www.texasstate.com/html/ger_pap1.ppt

The Aging Liver

The aging human liver appears to preserve its morphology and function relatively well. The liver appears to progressively decrease in both mass and volume. It also appears browner (a condition called "brown atrophy"), as a result of accumulation of lipofuscin (ceroid) within hepatocytes. Increases occur in the number of macrohepatocytes, and in polyploidy, especially around the terminal hepatic veins. The number of mitochondria declines, and both the rough and smooth endoplasmic reticulum diminish. The number of lysozymes increase.

The liver is the premiere metabolic organ of the body. With regard to metabolism, hepatic glycerides and cholesterol levels increase with age, at least up to age 90. On the other hand, phospholipids, aminotransferases, and serum bilirubin appear to remain normal. There are contradictory reports as to the effect of aging on albumin, serum gamma-glutamyltransferase, and hepatic alkaline phosphatase. It is worth noting that it has been shown that the content of cytochrome oxidase exhibits a progressive decline which correlates with age-associated decline in mtRNA synthesis in brain, liver, heart, lungs and skeletal muscle.

See generally Anantharaju, Feller and Chedid, "Aging Liver: A Review," *Gerontology*, 48: 343-53 (2002).

Aging Skeletal Muscle

Aging affects human skeletal muscle in a number of ways. One of the principal changes in muscle function is that the force-generating capacity (strength) of the muscles is reduced. This, in turn, can lead to problems in performing normal daily activities.

This loss of strength, in turn, is at least in part attributable to muscle atrophy, and alterations in the percentage of contractile tissue within muscle. The atrophy can be characterized as a decrease in the cross-sectional area of the muscle (sarcopenia). Sarcopenia can result from reductions in fiber size and/or fiber number; the latter appears to be the more important of the two. Also, it appears that the number of both type I (slow) and type II (fast) fibers is reduced, although the changes in the individual fibers are more pronounced in the case of type II fibers. The effects of aging on skeletal muscle may

be determined, inter alia, by measurements on whole muscle, or on individual muscle fibers.

Older people have fewer motor units, but this is usually compensated for through increases in the size of the remaining motor units. There is a difference of opinion as to the effect of age on MU firing rates. They may decrease with age, or they may simply become more variable.

Muscle mass also decreases with age. The muscle mass is determined by the relative rates of protein synthesis and breakdown, and it appears that with age, the rate of synthesis of at least some muscle proteins declines. The percentage of muscle mass which is contractile tissue also decreases with age. (Non-contractile tissue includes, e.g., connective tissue).

There may also be a reduction in intrinsic muscle function (the mechanisms by which a given mass of muscles produces force), perhaps as a result, at least in part, of an alteration in the sarcoplasmic reticulum.

Muscle performance may be a function of changes, not only in the muscle per se, but also other systems, such as the nervous and circulatory systems. However, Olive et al. did not observe age-related changes in maximal blood flow capacity after exercise, in resting blood flow, or in resting vascular diameter.

For more particulars, see Williams, GN, Higgins, MJ, Lewek, MD, "Aging Skeletal Muscle: Physiologic Changes and the effects of Training, " Physical Therapy 82: 62-68 (2002); Larson L and Ramamurthy B, "Aging-Related Changes in Skeletal

Muscle: Mechanisms and Interventions, Drugs and Aging 17: 303-16 (2000); ; Olive et al., "The effect of aging and activity on muscle blood flow," Dyn. Med. 1(1): 2 (Dec. 19, 2002).

It is within the contemplation of the invention to address one or more of these age-related changes in skeletal muscle, especially when the "favorable" or "unfavorable" gene/protein in question is one differentially expressed in skeletal muscle as a consequence of age.

Quality of Life

Clinicians are interested, not only in simple prolongation of lifespan, but also in maintenance of a high quality of life (QOL) over as much as possible of that lifespan. QOL can be defined subjectively in terms of the subject's satisfaction with life, or objectively in terms of the subject's physical and mental ability (but not necessarily willingness) to engage in "valued activities", such as those which are pleasurable or financially rewarding.

Flanagan has defined five domains of QOL, capturing 15 dimensions of life quality. The five domains, and their component dimensions, are physical and material well being (Material well-being and financial security; Health and personal safety), Relations with other people (relations with spouse; Having and rearing children; Relations with parents, siblings, or other

relatives ; Relations with friends) Social, community, civic activities (Helping and encouraging others; Participating in local and governmental affairs), Personal development, fulfillment (Intellectual development; Understanding and planning; Occupational role career;

Creativity and personal expression), and recreation (Socializing with others; Passive and observational recreational activities; Participating in active recreation). See Flanagan JC, "A research approach to improving our quality of life." Am Psychol 33:138-147 (1978).

"Health-related quality of life" (HRQL or HRQOL) is an individual's satisfaction or happiness with domains of life insofar as they affect or are affected by "health".

In a preferred embodiment, a pharmaceutical agent of the present invention is able to achieve a statistically significant improvement in the expected quality of life, measured according to a commonly accepted measure of QOL, in a treatment group over a control group.

While there is general acceptance of the notion that QOL is important, quantifying QOL is not especially straightforward. Also, QOL can only be measured in humans. Measurements of QOL can be objective (e.g., employment status, marital status, home ownership) or subjective (the subject's opinion of his or her life), or some combination of the two.

A simple approach to measuring subjective QOL is to simply have the subjects rate their overall quality of life on a scale, e.g., of 7 points. One can also use more elaborate measure, such as the Older Adult Health and Mood Questionnaire (a 22 item test for assessing depression). Objective QOL can be measured by, e.g., an activities checklist.

There is a relationship between QOL assessment and so-called ADL or IADL measures, which assess the need for assistance.

The Katz Index of Independence in Activities of Daily Living (Katz ADL) measures adequacy of independent performance of bathing, dressing, toileting, transferring, continence, and feeding. See Katz, S., "Assessing Self-Maintenance: Activities of Daily Living, Mobility and Instrumental Activities of Daily Living, Journal of the American Geriatrics Society, 31(12); 721-726 (1983); Katz S., Down, T.D., Cash, H.R. et al. Progress in the Development of the Index of ADL. Gerontologist, 10:20-30 (1970).

Performance of a more sophisticated nature is measured by the "Instrumental Activities of Daily Living" (IADL) scale. This inquires into ability to independently use the telephone, shop, prepare food, carry out housekeeping, do laundry, travel locally, take medication and handle finances. See Lawton, MP and Brody, EM, Gerontologist, 9:179-86 (1969).

The 36 question Medical Outcomes Study Short Form (SF-36) (Medical Outcomes Trust, Inc., 20 Park Plaza, Suite 1014, Boston, Massachusetts 02116) assesses eight health concepts: 1) limitations in physical activities because of health problems; 2) limitations in social activities because of physical or emotional problems; 3) limitations in usual role activities because of physical health problems; 4) bodily pain; 5) general mental health (psychological distress and well-being); 6) limitations in usual role activities because of emotional problems; 7) vitality (energy and fatigue); and 8) general health perceptions.

A low score on an ADL, IADL or SF-36 test is likely to be associated with a low QOL, but a high score does not guarantee a high QOL because these tests do not explore

performance of "valued activities", only of more basic activities. Nonetheless, these tests can be considered commonly accepted measures of QOL for the purpose of this invention.

Age-Related Diseases

Age-related (senescent) diseases include certain cancers, atherosclerosis, diabetes (type 2), osteoporosis, hypertension, depression, Alzheimer's, Parkinson's, glaucoma, certain immune system defects, kidney failure, and liver steatosis. In general, they are diseases for which the relative risk (comparing a subpopulation over age 55 to a suitably matched population under age 55) is at least 1.1.

Preferably, the agents of the present invention protect against one or more age-related diseases for at least a subpopulation of mature (post-puberty) adult subjects.

Diabetes

Type II diabetes is of particular interest. A deficiency of insulin in the body results in diabetes mellitus, which affects about 18 million individuals in the United States. It is characterized by a high blood glucose (sugar) level and glucose spilling into the urine due to a deficiency of insulin. As more glucose concentrates in the urine, more water is excreted, resulting in extreme thirst, rapid weight loss, drowsiness, fatigue, and possibly dehydration. Because the cells of the diabetic cannot use glucose for fuel, the body uses stored protein and fat for energy, which leads to a buildup of acid (acidosis) in the blood. If this condition is prolonged, the person can fall into a diabetic coma, characterized by deep labored breathing and fruity-odored breath.

There are two types of diabetes mellitus, Type I and Type II. Type II diabetes is the predominant form found in the Western world; fewer than 8% of diabetic Americans have the type I disease.

Type I diabetes. In Type I diabetes, formerly called juvenile-onset or insulin-dependent diabetes mellitus, the pancreas cannot produce insulin. People with Type I diabetes must have daily insulin injections. But they need to avoid taking too much insulin because that can lead to insulin shock, which begins with a mild hunger. This is quickly followed by sweating, shallow breathing, dizziness, palpitations, trembling, and mental confusion. As the blood sugar falls, the body tries to compensate by breaking down fat and protein to make more sugar. Eventually, low blood sugar leads to a decrease in the sugar supply to the brain, resulting in a loss of consciousness. Eating a sugary food can prevent insulin shock until appropriate medical measures can be taken.

Type I diabetics are often characterized by their low or absent levels of circulating endogenous insulin; i.e., hypoinsulinemia (1). Islet cell antibodies causing damage to the pancreas are frequently present at diagnosis. Injection of exogenous insulin is required to prevent ketosis and sustain life.

Type II diabetes. Type II diabetes, formerly called adult-onset or non-insulin-dependent diabetes mellitus (NIDDM), can occur at any age. The pancreas can produce insulin, but the cells do not respond to it.

Type II diabetes is a metabolic disorder that affects approximately 17 million Americans. It is estimated that another 10 million individuals are "prone" to becoming diabetic. These vulnerable individuals can become resistant

to insulin, a pancreatic hormone that signals glucose (blood sugar) uptake by fat and muscle. In order to maintain normal glucose levels, the islet cells of the pancreas produce more insulin, resulting in a condition called hyperinsulinemia. When the pancreas can no longer produce enough insulin to compensate for the insulin resistance, and thereby maintain normal glucose levels, hyperglycemia (elevated blood glucose) results, and type II diabetes is diagnosed.

Early Type II diabetics are often characterized by hyperinsulinemia and resistance to insulin. Late Type II diabetics may be normoinsulinemic or hypoinsulinemic. Type II diabetics are usually not insulin dependent or prone to ketosis under normal circumstances.

Little is known about the disease progression from the normoinsulinemic state to the hyperinsulinemic state, and from the hyperinsulinemic state to the Type II diabetic state.

As stated above, type II diabetes is a metabolic disorder that is characterized by insulin resistance and impaired glucose-stimulated insulin secretion (2,3,4). However, Type II diabetes and atherosclerotic disease are viewed as consequences of having the insulin resistance syndrome (IRS) for many years (5). The current theory of the pathogenesis of Type II diabetes is often referred to as the "insulin resistance/islet cell exhaustion" theory. According to this theory, a condition causing insulin resistance compels the pancreatic islet cells to hypersecrete insulin in order to maintain glucose homeostasis. However, after many years of hypersecretion, the islet cells eventually fail and the symptoms of clinical diabetes are manifested. Therefore, this theory implies that, at some point, peripheral hyperinsulinemia will be an antecedent of Type II diabetes. Peripheral hyperinsulinemia

can be viewed as the difference between what is produced by the beta cell minus that which is taken up by the liver. Therefore, peripheral hyperinsulinemia can be caused by increased beta cell production, decreased hepatic uptake or some combination of both. It is also important to note that it is not possible to determine the origin of insulin resistance once it is established since the onset of peripheral hyperinsulinemia leads to a condition of global insulin resistance.

Multiple environmental and genetic factors are involved in the development of insulin resistance, hyperinsulinemia and type II diabetes. An important risk factor for the development of insulin resistance, hyperinsulinemia and type II diabetes is obesity, particularly visceral obesity (6,7,8). Type II diabetes exists world-wide, but in developed societies, the prevalence has risen as the average age of the population increases and the average individual becomes more obese.

Role of Muscle in Development of Type II Diabetes

Muscle, fat and liver tissues are the major contributors to the development of insulin resistance, hyperinsulinemia, and, ultimately, type II diabetes.

Muscle cells respond to insulin by increasing glucose uptake from the bloodstream. Muscle tissue can become resistant to insulin, causing the beta cells to initially increase insulin secretion. Eventually, though, the beta cells become unable to compensate for this increasing insulin resistance from muscle and other cells, and they fail to respond to elevated blood glucose levels. Thus, clinical type 2 diabetes results from the combination of insulin resistance and impaired beta cell function.

Defects in muscle glycogen synthesis are known to play a role in the development of insulin resistance. At least

three steps-those mediated by glycogen synthase, hexokinase, and GLUT4-have been reported to be defective in patients with type 2 diabetes.

Fatty acids can induce insulin resistance, and it has been suggested that this was a consequence of altered insulin signaling through PI3-kinase. PKC-theata has also been implicated.

See generally Petersen, et al., "Pathogenesis of Skeletal muscle insulin resistance in type 2 diabetes mellitus", in "A Symposium: Evolution of type 2 diabetes mellitus management", at *Amer. J. Cardiol.*, 90(5A): 11G-18G, (Sept. 5, 2002).

Adverse Effects of Type II Diabetes on Muscle

"Myopathy is a general term used to describe any disease of muscles, such as the muscular dystrophies and myopathies associated with thyroid disease. It can be caused by endocrine disorders, including diabetes, metabolic disorders, infection or inflammation of the muscle, certain drugs and mutations in genes. In diabetes, myopathy is thought to be caused by neuropathy, a complication of diabetes. General symptoms of myopathies include muscle weakness of limbs sometimes occurring during exercise although in some cases the symptoms diminish as exercise increases. Depending on the type of myopathy, one muscle group may be more affected than others." See "Joint and Muscle Problems Associated with Diabetes", www.iddtinternational.org/jointandmuscleproblems.html [Last modified June 12, 2003].

Diabetic muscle infarction can spontaneously affect patients with a long history of poorly controlled diabetes. "Most affected patients have multiple microvascular

complications (neuropathy, nephropathy, and retinopathy). The clinical presentation is an acute onset of pain and swelling over days to weeks in the affected muscle groups (usually the thigh or calf), along with varying degrees of tenderness.... Therapy consists of rest and analgesia. Routine daily activities are not deleterious to the condition, but physical therapy may cause exacerbation. Spontaneous diabetic muscle infarction tends to resolve over a period of weeks to months in most cases." See "Musculoskeletal Complications of Diabetes - Part 2", www.diabetic-lifestyle.com/articles/jan02_whats_1.htm [last modified Feb. 9, 2004]. See also Trujillo-Santos, et al., "Diabetes muscle infarction: an underdiagnosed complication of long-standing diabetes," *Diabetes Care*, 26(1):211-5 (2003).

Diseases Characterized by Accelerated Aging

Several human diseases display some features of accelerated aging. These include Werner's syndrome (classic early-onset progeria), Hutchinson-Gilford syndrome (adult progeria), and Down's syndrome (trisomy 21). Troen, *Biology of Aging*, Mt. Sinai J. Med., 70(1): 3 (Jan. 2003). Thus, the present invention may be useful in the treatment (curative or ameliorative) of individuals with these diseases.

Direct and Indirect Utility of Identified Nucleic Acid Sequences and Related Molecules

The identified mouse or human genes may be used directly. For diagnostic or screening purposes, they (or specific binding fragments thereof) may be labeled and used as hybridization probes. For therapeutic purposes, they (or

specific binding fragments thereof) may be used as antisense reagents to inhibit the expression of the corresponding gene, or of a sufficiently homologous gene of another species.

If the database DNA appears to be a full-length cDNA or gDNA, that is, that it encodes an entire, functional, naturally occurring protein, then it may be used in the expression of that protein. Such expression may be in cell culture, with the protein subsequently isolated and administered exogenously to subjects who would benefit therefrom, or in vivo, i.e., administration by gene therapy. Naturally, any DNA encoding the same protein may be used for the same purpose, and a DNA encoding a protein which a fragment or a mutant of that naturally occurring protein which retains the desired activity, may be used for the purpose of producing the active fragment or mutant. The encoded protein of course has utility therapeutically and, in labeled or immobilized form, diagnostically.

The genes may also be used indirectly, that is, to identify other useful DNAs, proteins, or other molecules. We have attempted to determine whether the mouse genes disclosed herein have significant similarity to any known human DNA, and whether, in any of the six possible combinations of reference frame and strand, they encode a protein similar to a known human protein. If so, then it follows that the known human protein, and DNAs encoding that protein, may be used in a similar manner. In addition, if the known human protein is known to have additional homologues, then those homologous proteins, and DNAs encoding them, may be used in a similar manner.

There thus are several ways that a human protein homologue of interest can be identified by database searching, including but not limited to:

- 1) a DNA->DNA (BlastN) search for human database DNAs closely related to the mouse gene identifies a known human gene, and the sequence of the human protein is deduced by the Genetic Code;
- 2) a DNA->Protein (BlastX) search for human database proteins closely related to the translated DNA of the mouse gene identifies a known human protein; and
- 3) the sequence of the mouse protein is known or deduced by the Genetic Code, and a Protein->Protein (BlastP) search for closely related database proteins identifies a known human protein.

Once a known human gene is identified, it may be used in further BlastN or BlastX searches to identify other human genes or proteins. Once a known human protein is identified, it may be used in further BlastP searches to identify other human proteins. Searches may also take cognizance, intermediately, of known genes and proteins other than mouse or human ones, e.g., use the mouse sequence to identify a known rat sequence and then the rat sequence to identify a human one.

If we have identified a mouse gene, and it encodes a mouse protein which appears similar to a human protein, then that human protein may be used (especially in humans) for purposes analogous to the proposed use of the mouse protein in mice. Moreover, a specific binding fragment of an appropriate strand of the corresponding human gene (gDNA or

cDNA) could be labeled and used as a hybridization probe (especially against samples of human mRNA or cDNA).

In determining whether the disclosed genes (gDNA or cDNA) have significant similarities to known DNAs (and their translated AA sequences to known proteins), one would generally use the disclosed gene as a query sequence in a search of a sequence database. The results of several such searches are set forth in the Examples. Such results are dependent, to some degree, on the search parameters. Preferred parameters are set forth in Example 1. The results are also dependent on the content of the database. While the raw similarity score of a particular target (database) sequence will not vary with content (as long as it remains in the database), its informational value (in bits), expected value, and relative ranking can change. Generally speaking, the changes are small.

It will be appreciated that the nucleic acid and protein databases keep growing. Hence a later search may identify high scoring target sequences which were not uncovered by an earlier search because the target sequences were not previously part of a database.

Hence, in a preferred embodiment, the cognate DNAs and proteins include not only those set forth in the examples, but those which would have been highly ranked (top ten, more preferably top three, even more preferably top two, most preferably the top one) in a search run with the same parameters on the date of filing of this application.

If the mouse or human database DNA appears to be a partial sequence (that is, partial relative to a cDNA or gDNA encoding the whole naturally occurring protein), it may be used as a hybridization probe to isolate the full-length

DNA. If the partial DNA sequence encodes a biologically functional fragment of the cognate protein, it may be used in a manner similar to the full length DNA, i.e., to produce the functional fragment.

If we have indicated that an antagonist of a protein or other molecule is useful, then such an antagonist may be obtained by preparing a combinatorial library, as described below, of potential antagonists, and screening the library members for binding to the protein or other molecule in question. The binding members may then be further screened for the ability to antagonize the biological activity of the target. The antagonists may be used therapeutically, or, in suitably labeled or immobilized form, diagnostically.

If the mouse or human database DNA is related to a known protein, then substances known to interact with that protein (e.g., agonists, antagonists, substrates, receptors, second messengers, regulators, and so forth), and binding molecules which bind them, are also of utility. Such binding molecules can likewise be identified by screening a combinatorial library.

Isolation of Full Length DNAs Using Partial DNAs as probes

If it is determined that a DNA of the present invention is a partial DNA, and the cognate full length DNA is not listed in a sequence database, the available DNA may be used as a hybridization probe to isolate the full-length DNA from a suitable DNA library (cDNA or gDNA).

Stringent hybridization conditions are appropriate, that is, conditions in which the hybridization temperature is 5-10 deg. C. below the T_m of the DNA as a perfect duplex.

Identification and Isolation of Homologous Genes Using a DNA Probe

It may be that the sequence databases available do not include the sequence of any homologous gene (cDNA or gDNA), or at least of the homologous gene for a species of interest. However, given the DNAs set forth above, one may readily obtain the homologous gene.

The possession of one DNA (the "starting DNA") greatly facilitates the isolation of homologous DNAs. If the clone in question only features a partial DNA, this partial DNA may first be used as a probe to isolate the corresponding full length DNA for the same species, and that the latter may be used as the starting DNA in the search for homologous DNAs.

The starting DNA, or a fragment thereof, is used as a hybridization probe to screen a cDNA or genomic DNA library for clones containing inserts which encode either the entire homologous protein, or a recognizable fragment thereof. The minimum length of the hybridization probe is dictated by the need for specificity. If the size of the library in bases is L , and the GC content is 50%, then the probe should have a length of at least l , where $L = 4^l$. This will yield, on average, a single perfect match in random DNA of L bases. The human cDNA library is about 10^8 bases and the human genomic DNA library is about 10^{10} bases.

The library is preferably derived from an organism which is known, on biochemical evidence, to produce a homologous protein, and more preferably from the genomic DNA or mRNA of cells of that organism which are likely to be relatively high producers of that protein. A cDNA library (which is derived from an mRNA library) is especially preferred.

If the organism in question is known to have substantially different codon preferences from that of the

organism whose relevant cDNA or genomic DNA is known, a synthetic hybridization probe may be used which encodes the same amino acid sequence but whose codon utilization is more similar to that of the DNA of the target organism. Alternatively, the synthetic probe may employ inosine as a substitute for those bases which are most likely to be divergent, or the probe may be a mixed probe which mixes the codons for the source DNA with the preferred codons (encoding the same amino acid) for the target organism.

By routine methods, the T_m of a perfect duplex of starting DNA is determined. One may then select a hybridization temperature which is sufficiently lower than the perfect duplex T_m to allow hybridization of the starting DNA (or other probe) to a target DNA which is divergent from the starting DNA. A 1% sequence divergence typically lowers the T_m of a duplex by 1-2°C, and the DNAs encoding homologous proteins of different species typically have sequence identities of around 50-80%. Preferably, the library is screened under conditions where the temperature is at least 20°C., more preferably at least 50°C., below the perfect duplex T_m . Since salt reduces the T_m , one ordinarily would carry out the search for DNAs encoding highly homologous proteins under relatively low salt hybridization conditions, e.g., <1M NaCl. The higher the salt concentration, and/or the lower the temperature, the greater the sequence divergence which is tolerated.

For the use of probes to identify homologous genes in other species, see, e.g., Schwinn, et al., J. Biol. Chem., 265:8183-89 (1990) (hamster 67-bp cDNA probe vs. human leukocyte genomic library; human 0.32kb DNA probe vs. bovine brain cDNA library, both with hybridization at 42°C in 6xSSC); Jenkins et al., J. Biol. Chem., 265:19624-31 (1990) (Chicken 770-bp cDNA probe vs. human genomic libraries; hybridization at 40°C in 50% formamide and 5xSSC); Murata et

al., J. Exp. Med., 175:341-51 (1992) (1.2-kb mouse cDNA probe v. human eosinophil cDNA library; hybridization at 65°C in 6xSSC); Guyer et al., J. Biol. Chem., 265:17307-17 (1990) (2.95-kb human genomic DNA probe vs. porcine genomic DNA library; hybridization at 42°C in 5xSSC). The conditions set forth in these articles may each be considered suitable for the purpose of isolating homologous genes.

Corresponding (Homologous) Proteins and DNAs

In the case of a gene chip, the manufacturer of the gene chip determines which DNA to place at each position on the chip. This DNA may correspond in sequence to a genomic DNA, a cDNA, or a fragment of genomic or cDNA, and may be natural, synthetic or partially natural and partially synthetic in origin. The manufacturer of the gene chip will normally identify the DNA for a mouse gene chip as corresponding to a particular mouse gene, in which case it will be assumed that the alignments of chip DNA to mouse gene satisfies the homology criteria of the invention.

Usually, the gene chip manufacturer will provide a sequence database accession number for the mouse DNA. If so, to identify the corresponding mouse protein, we will first inspect the database record for that mouse DNA. Often, the mouse protein accession number will appear in that record or in a linked record. If it doesn't, the corresponding mouse protein can be identified by performing a BlastX search on a mouse protein database with the mouse database DNA sequence as the query sequence. Even if the protein sequence is not in the database, if the DNA sequence comprises a full-length coding sequence, the corresponding protein can be identified by translating the coding sequence in accordance with the Genetic Code.

A human protein can be said to be identifiable as corresponding (homologous) to a gene chip DNA if it is identified as corresponding (homologous) to the mouse gene (gDNA or cDNA, whole or partial) identified by the gene chip manufacturer as corresponding to that gene chip DNA.

In turn, it is identifiable as corresponding (homologous) to said identified mouse gene, if

- (1) it can be aligned by BlastX directly to that mouse gene, and/or
- (2) it is encoded by a human gene, or can be aligned to a human gene by BlastX, which in turn can be aligned by BlastN to said mouse gene and/or
- (3) it can be aligned by BlastP to a mouse protein, the latter being encoded by said mouse gene, or aligned to said mouse gene BlastX,

where any alignment by BlastN, BlastP or BlastX is in accordance with the default parameters set forth below, and the expected value (E) of each alignment (the probability that such an alignment would have occurred by chance alone) is less than e^{-10} . (Note that because this is a negative exponent, a value such as e^{-50} is less than e^{-10} .)

Desirably, two or all three of these conditions (1)-(3) are satisfied for the corresponding (homologous) human genes and proteins.

A human gene is corresponding (homologous) to a mouse gene chip DNA, and hence to said identified mouse gene (or cDNA) and protein, if it encodes a corresponding

(homologous) human protein as defined above, or it can be aligned by BlastN to said mouse gene.

Preferably, for at least one of conditions (1)-(3), the E value is less than e-50, more preferably less than e-60, still more preferably less than e-70, even more preferably less than e-80, considerably more preferably less than e-90, and most preferably less than e-100. Desirably, it is true for two or even all three of these conditions.

In constructing Master table 1, we generally used a BlastX (mouse gene vs. human protein) alignment E value cutoff of e-50. However, if there were no human proteins with that good an alignment to the mouse DNA in question, or if there were other reasons for including a particular human protein (e.g., a known functionality supportive of the observed differential cognate mouse protein expression), then a human protein with a score worse (i.e., higher) than e-50 may appear in Master Table 1.

If the manufacturer of the gene chip identifies the gene chip DNA as corresponding to an EST, or other DNA which is not a full-length mouse gene or cDNA, a longer (possibly full length) mouse gene or cDNA may be identified by a BlastN search of the mouse DNA database. Alternatively, the identified DNA may be used to conduct a BlastN search of a human DNA database, or a BlastX search of a mouse or human protein database.

Thus, more generally, a human protein can be said to be identifiable as corresponding (homologous) to a gene chip DNA, or to a DNA identified by the manufacturer as corresponding to that gene chip DNA, if

(1') it can be aligned directly to the gene chip or corresponding manufacturer identified DNA by BlastX. and/or

(2') it can be aligned to a human gene/cDNA by BlastX, whose genomic DNA (gDNA) or cDNA (DNA complementary to messenger RNA) in turn can be aligned to the gene chip or corresponding manufacturer identified DNA by BlastN, and/or

(3') it can be aligned to a mouse gene/cDNA by BlastX, whose gDNA or cDNA in turn can be aligned to the gene chip or corresponding manufacturer identified DNA by BlastN, and/or

(4') it can be aligned to a mouse protein by BlastP, which in turn can be aligned to the gene chip or corresponding manufacturer identified DNA by BlastX, and/or

(5') it can be aligned to a mouse protein by BlastP, which in turn can be aligned to a mouse gene/cDNA by BlastX, whose gDNA or cDNA can in turn be aligned to the gene chip or corresponding manufacturer identified DNA by BlastN;

where any alignment by BlastN, BlastP, or BlastX is in accordance with the default parameters set forth below, and the expected value (E) of each alignment (the probability that such an alignment would have occurred by chance alone) is less than e^{-10} . (Note that because this is a negative exponent, a value such as e^{-50} is less than e^{-10} .)

Preferably, two, three, four or all five of conditions (1')-(5') are satisfied.

Preferably, for at least one of conditions (1')-(5'), for at least the final alignment (i.e., vs. the human protein), the E value is less than e^{-50} , more preferably less than e^{-60} , , still more preferably less than e^{-70} , even more preferably less than e^{-80} , considerably more preferably less than e^{-90} , and most preferably less than e^{-100} .

Desirably, one or more of these standards of preference are met for two, three, four or all five of conditions (1')-(5'). In particular, for those conditions in which the gene chip or corresponding manufacturer identified DNA is indirectly connected to the human protein by virtue of two or more successive alignments, the E value is preferably, so limited for all of said alignments in the connecting chain.

A human gene corresponds (is homologous) to a gene chip DNA or manufacturer identified corresponding DNA if it encodes a homologous human protein as defined above, or if it can be aligned either directly to that DNA, or indirectly through a mouse gene which can be aligned to said DNA, according to the conditions set forth above.

Master table 1 assembles a list of human protein corresponding to each of the mouse DNAs/proteins identified as related to the chip DNA. These human proteins form a set and can be given a percentile rank, with respect to E value, within that set. The human proteins of the present invention preferably are those scorers with a percentile rank of at least 50%, more preferably at least 60%, still more preferably at least 70%, even more preferably at least 80%, and most preferably at least 90%.

For each mouse gene/cDNA in Master Table 1, there is a particular human protein which provides the best alignment match as measured by BlastX, i.e., the human protein with the best score (lowest e-value). These human proteins form a subset of the set above and can be given a percentile rank within that subset, e.g., the human proteins with scores in the top 10% of that subset have a percentile rank of 90% or higher.

The human proteins of the present invention preferably are those best scorer subset proteins with a percentile rank within the subset of at least 50%, more preferably at least 60%, still more preferably at least 70%, even more preferably at least 80%, and most preferably at least 90%.

BlastN and BlastX report very low expected values as "0.0". This does not truly mean that the expected value is exactly zero (since any alignment could occur by chance), but merely that it is so infinitesimal that it is not reported. The documentation does not state the cutoff value, but alignments with explicit E values as low as e^{-178} (624 bits) have been reported as nonzero values, while a score of 636 bits was reported as "0.0".

Functionally homologous human proteins are also of interest. A human protein may be said to be functionally homologous to the mouse gene if the human protein has at least one biological activity in common with the mouse protein encoded by said mouse gene.

The human proteins of interest also include those that are substantially and/or conservatively identical (as defined below) to the homologous and/or functionally homologous human proteins defined above.

Degree of Differential Expression

The degree of differential expression may be expressed as the ratio of the higher expression level to the lower expression level. Preferably, this is at least 2-fold, and more preferably, it is higher, such as at least 3-fold, at least 4-fold, at least 5-fold, at least 6-fold, at least 7-fold, at least 8-fold, at least 9-fold, or at least 10-fold.

Most preferably, the human protein of interest corresponds to a mouse gene for which the degree of differential expression places it among the top 10% of the mouse genes in the appropriate subtable.

Relevance of Favorable and Unfavorable Genes

If a gene is down-regulated in more favored mammals, or up-regulated in less favored mammals, (i.e., an "unfavorable gene") then several utilities are apparent.

First, the complementary strand of the gene, or a portion thereof, may be used in labeled form as a hybridization probe to detect messenger RNA and thereby monitor the level of expression of the gene in a subject. Elevated levels are indicative of progression, or propensity to progression, to a less favored state, and clinicians may take appropriate preventative, curative or ameliorative action.

Secondly, the messenger RNA product (or equivalent cDNA), the protein product, or a binding molecule specific for that product (e.g., an antibody which binds the product), or a downstream product which mediates the activity (e.g., a signaling intermediate) or a binding molecule (e.g., an antibody) therefor, may be used, preferably in labeled or immobilized form, as an assay reagent in an assay for said nucleic acid product, protein product, or downstream product (e.g., a signaling intermediate). Again, elevated levels are indicative of a present or future problem.

Thirdly, an agent which down-regulates expression of the gene may be used to reduce levels of the corresponding protein and thereby inhibit further damage. This agent could inhibit transcription of the gene in the subject, or translation of the corresponding messenger RNA. Possible inhibitors of transcription and translation include antisense molecules and repressor molecules. The agent could also inhibit a post-translational modification (e.g., glycosylation, phosphorylation, cleavage, GPI attachment) required for activity, or post-translationally modify the protein so as to inactivate it. Or it could be an agent which down- or up-regulated a positive or negative regulatory gene, respectively.

Fourthly, an agent which is an antagonist of the messenger RNA product or protein product of the gene, or of a downstream product through which its activity is manifested (e.g., a signaling intermediate), may be used to inhibit its activity. This antagonist could be an antibody, a peptide, a peptoid, a nucleic acid, a peptide nucleic acid (PNA) oligomer, a small organic molecule of a kind for which a combinatorial library exists (e.g., a benzodiazepine), etc. An antagonist is simply a binding molecule which, by binding, reduces or abolishes the undesired activity of its target. The antagonist, if not an oligomeric molecule, is preferably less than 1000 daltons, more preferably less than 500 daltons.

Fifthly, an agent which degrades, or abets the degradation of, that messenger RNA, its protein product or a downstream product which mediates its activity (e.g., a signaling intermediate), may be used to curb the effective period of activity of the protein.

If a gene is up-regulated in more favored mammals, or down-regulated in less favored animals then the utilities are converse to those stated above.

First, the complementary strand of the gene, or a portion thereof, may be used in labeled form as a hybridization probe to detect messenger RNA and thereby monitor the level of expression of the gene in a subject. Depressed levels are indicative of damage, or possibly of a propensity to damage, and clinicians may take appropriate preventative, curative or ameliorative action.

Secondly, the messenger RNA product, the equivalent cDNA, protein product, or a binding molecule specific for those products, or a downstream product, or a signaling intermediate, or a binding molecule therefor, may be used, preferably in labeled or immobilized form, as an assay reagent in an assay for said protein product or downstream product. Again, depressed levels are indicative of a present or future problem.

Thirdly, an agent which up-regulates expression of the gene may be used to increase levels of the corresponding protein and thereby inhibit further progression to a less favored state. By way of example, it could be a vector which carries a copy of the gene, but which expresses the gene at higher levels than does the endogenous expression system. Or it could be an agent which up- or down-regulates a positive or negative regulatory gene.

Fourthly, an agent which is an agonist of the protein product of the gene, or of a downstream product through which its activity (of inhibition of progression to a less favored state) is manifested, or of a signaling intermediate may be used to foster its activity.

Fifthly, an agent which inhibits the degradation of that protein product or of a downstream product or of a signaling intermediate may be used to increase the effective period of activity of the protein.

Mutant Proteins

The present invention also contemplates mutant proteins (peptides) which are substantially identical (as defined below) to the parental protein (peptide). In general, the fewer the mutations, the more likely the mutant protein is to retain the activity of the parental protein. The effect of mutations is usually (but not always) additive. Certain individual mutations are more likely to be tolerated than others.

A protein is more likely to tolerate a mutation which

(a) is a substitution rather than an insertion or deletion;

(b) is an insertion or deletion at the terminus, rather than internally, or, if internal, is at a domain

boundary, or a loop or turn, rather than in an alpha helix or beta strand;

(c) affects a surface residue rather than an interior residue;

(d) affects a part of the molecule distal to the binding site;

(e) is a substitution of one amino acid for another of similar size, charge, and/or hydrophobicity, and does not destroy a disulfide bond or other crosslink; and

(f) is at a site which is subject to substantial variation among a family of homologous proteins to which the protein of interest belongs.

These considerations can be used to design functional mutants.

Surface vs. Interior Residues

Charged amino acid residues almost always lie on the surface of the protein. For uncharged residues, there is less certainty, but in general, hydrophilic residues are partitioned to the surface and hydrophobic residues to the interior. Of course, for a membrane protein, the membrane-spanning segments are likely to be rich in hydrophobic residues.

Surface residues may be identified experimentally by various labeling techniques, or by 3-D structure mapping techniques like X-ray diffraction and NMR. A 3-D model of a homologous protein can be helpful.

Binding Site Residues

Residues forming the binding site may be identified by (1) comparing the effects of labeling the surface residues before and after complexing the protein to its target, (2) labeling the binding site directly with affinity ligands, (3) fragmenting the protein and testing the fragments for binding activity, and (4) systematic mutagenesis (e.g., alanine-scanning mutagenesis) to determine which mutants destroy binding. If the binding site of a homologous protein is known, the binding site may be postulated by analogy.

Protein libraries may be constructed and screened that a large family (e.g., 10^8) of related mutants may be evaluated simultaneously.

Hence, the mutations are preferably conservative modifications as defined below.

"Substantially Identical"

A mutant protein (peptide) is substantially identical to a reference protein (peptide) if (a) it has at least 10% of a specific binding activity or a non-nutritional biological activity of the reference protein, and (b) is at least 50% identical in amino acid sequence to the reference protein (peptide). It is "substantially structurally identical" if condition (b) applies, regardless of (a).

Percentage amino acid identity is determined by aligning the mutant and reference sequences according to a rigorous dynamic programming algorithm which globally aligns their sequences to maximize their similarity, the similarity being scored as the sum of scores for each aligned pair according to an unbiased PAM250 matrix, and a penalty for each internal gap of -12 for the first null of the gap and -4 for each additional null of the same gap. The percentage identity is the number of matches expressed as a percentage of the adjusted (i.e., counting inserted nulls) length of the reference sequence.

A mutant DNA sequence is substantially identical to a reference DNA sequence if they are structural sequences, and encoding mutant and reference proteins which are substantially identical as described above.

If instead they are regulatory sequences, they are substantially identical if the mutant sequence has at least 10% of the regulatory activity of the reference sequence, and is at least 50% identical in nucleotide sequence to the reference sequence. Percentage identity is determined as for proteins except that matches are scored +5, mismatches -4, the gap open penalty is -12, and the gap extension penalty (per additional null) is -4.

More preferably, the sequence is not merely substantially identical, but rather is at least 51%, 66%,

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75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical in sequence to the reference sequence.

DNA sequences may also be considered "substantially identical" if they hybridize to each other under stringent conditions, i.e., conditions at which the T_m of the heteroduplex of the one strand of the mutant DNA and the more complementary strand of the reference DNA is not in excess of 10°C. less than the T_m of the reference DNA homoduplex. Typically this will correspond to a percentage identity of 85-90%.

"Conservative Modifications"

"Conservative modifications" are defined as

- (a) conservative substitutions of amino acids as hereafter defined; or
- (b) single or multiple insertions (extension) or deletions (truncation) of amino acids at the termini.

Conservative modifications are preferred to other modifications. Conservative substitutions are preferred to other conservative modifications.

"Semi-Conservative Modifications" are modifications which are not conservative, but which are (a) semi-conservative substitutions as hereafter defined; or (b) single or multiple insertions or deletions internally, but at interdomain boundaries, in loops or in other segments of relatively high mobility. Semi-conservative modifications are preferred to nonconservative modifications. Semi-conservative substitutions are preferred to other semi-conservative modifications.

Non-conservative substitutions are preferred to other non-conservative modifications.

The term "conservative" is used here in an a priori sense, i.e., modifications which would be expected to preserve 3D structure and activity, based on analysis of the

naturally occurring families of homologous proteins and of past experience with the effects of deliberate mutagenesis, rather than post facto, a modification already known to conserve activity. Of course, a modification which is conservative a priori may, and usually is, also conservative post facto.

Preferably, except at the termini, no more than about five amino acids are inserted or deleted at a particular locus, and the modifications are outside regions known to contain binding sites important to activity.

Preferably, insertions or deletions are limited to the termini.

A conservative substitution is a substitution of one amino acid for another of the same exchange group, the exchange groups being defined as follows.

- I Gly, Pro, Ser, Ala (Cys) (and any nonbiogenic, neutral amino acid with a hydrophobicity not exceeding that of the aforementioned a.a.'s)
- II Arg, Lys, His (and any nonbiogenic, positively-charged amino acids)
- III Asp, Glu, Asn, Gln (and any nonbiogenic negatively-charged amino acids)
- IV Leu, Ile, Met, Val (Cys) (and any nonbiogenic, aliphatic, neutral amino acid with a hydrophobicity too high for I above)
- V Phe, Trp, Tyr (and any nonbiogenic, aromatic neutral amino acid with a hydrophobicity too high for I above).

Note that Cys belongs to both I and IV.

Residues Pro, Gly and Cys have special conformational roles. Cys participates in formation of disulfide bonds. Gly imparts flexibility to the chain. Pro imparts rigidity to the chain and disrupts α helices. These residues may be

essential in certain regions of the polypeptide, but substitutable elsewhere.

One, two or three conservative substitutions are more likely to be tolerated than a larger number.

"Semi-conservative substitutions" are defined herein as being substitutions within supergroup I/II/III or within supergroup IV/V, but not within a single one of groups I-V. They also include replacement of any other amino acid with alanine. If a substitution is not conservative, it preferably is semi-conservative.

"Non-conservative substitutions" are substitutions which are not "conservative" or "semi-conservative".

"Highly conservative substitutions" are a subset of conservative substitutions, and are exchanges of amino acids within the groups Phe/Tyr/Trp, Met/Leu/Ile/Val, His/Arg/Lys, Asp/Glu and Ser/Thr/Ala. They are more likely to be tolerated than other conservative substitutions. Again, the smaller the number of substitutions, the more likely they are to be tolerated.

"Conservatively Identical"

A protein (peptide) is conservatively identical to a reference protein (peptide) if it differs from the latter, if at all, solely by conservative modifications, the protein (peptide) remaining at least seven amino acids long if the reference protein (peptide) was at least seven amino acids long.

A protein is at least semi-conservatively identical to a reference protein (peptide) if it differs from the latter, if at all, solely by semi-conservative or conservative modifications.

A protein (peptide) is nearly conservatively identical to a reference protein (peptide) if it differs from the

latter, if at all, solely by one or more conservative modifications and/or a single nonconservative substitution.

It is highly conservatively identical if it differs, if at all, solely by highly conservative substitutions. Highly conservatively identical proteins are preferred to those merely conservatively identical. An absolutely identical protein is even more preferred.

The core sequence of a reference protein (peptide) is the largest single fragment which retains at least 10% of a particular specific binding activity, if one is specified, or otherwise of at least one specific binding activity of the referent. If the referent has more than one specific binding activity, it may have more than one core sequence, and these may overlap or not.

If it is taught that a peptide of the present invention may have a particular similarity relationship (e.g., markedly identical) to a reference protein (peptide), preferred peptides are those which comprise a sequence having that relationship to a core sequence of the reference protein (peptide), but with internal insertions or deletions in either sequence excluded. Even more preferred peptides are those whose entire sequence has that relationship, with the same exclusion, to a core sequence of that reference protein (peptide).

Library

The term "library" generally refers to a collection of chemical or biological entities which are related in origin, structure, and/or function, and which can be screened simultaneously for a property of interest.

Libraries may be classified by how they are constructed (natural vs. artificial diversity; combinatorial vs. noncombinatorial), how they are screened (hybridization, expression, display), or by the nature of the screened library members (peptides, nucleic acids, etc.).

In a "natural diversity" library, essentially all of the diversity arose without human intervention. This would be true, for example, of messenger RNA extracted from a non-engineered cell.

In a "synthetic diversity" library, essentially all of the diversity arose deliberately as a result of human intervention. This would be true for example of a combinatorial library; note that a small level of natural diversity could still arise as a result of spontaneous mutation. It would also be true of a noncombinatorial

library of compounds collected from diverse sources, even if they were all natural products.

In a "non-natural diversity" library, at least some of the diversity arose deliberately through human intervention.

In a "controlled origin" library, the source of the diversity is limited in some way. A limitation might be to cells of a particular individual, to a particular species, or to a particular genus, or, more complexly, to individuals of a particular species who are of a particular age, sex, physical condition, geographical location, occupation and/or familial relationship. Alternatively or additionally, it might be to cells of a particular tissue or organ. Or it could be cells exposed to particular pharmacological, environmental, or pathogenic conditions. Or the library could be of chemicals, or a particular class of chemicals, produced by such cells.

In a "controlled structure" library, the library members are deliberately limited by the production conditions to particular chemical structures. For example, if they are oligomers, they may be limited in length and monomer composition, e.g. hexapeptides composed of the twenty genetically encoded amino acids.

Hybridization Library

In a hybridization library, the library members are nucleic acids, and are screened using a nucleic acid hybridization probe. Bound nucleic acids may then be amplified, cloned, and/or sequenced.

Expression Library

In an expression library, the screened library members are gene expression products, but one may also speak of an underlying library of genes encoding those products. The library is made by subcloning DNA encoding the library members (or portions thereof) into expression vectors (or into cloning vectors which subsequently are used to construct expression vectors), each vector comprising an

expressible gene encoding a particular library member, introducing the expression vectors into suitable cells, and expressing the genes so the expression products are produced.

In one embodiment, the expression products are secreted, so the library can be screened using an affinity reagent, such as an antibody or receptor. The bound expression products may be sequenced directly, or their sequences inferred by, e.g., sequencing at least the variable portion of the encoding DNA.

In a second embodiment, the cells are lysed, thereby exposing the expression products, and the latter are screened with the affinity reagent.

In a third embodiment, the cells express the library members in such a manner that they are displayed on the surface of the cells, or on the surface of viral particles produced by the cells. (See display libraries, below).

In a fourth embodiment, the screening is not for the ability of the expression product to bind to an affinity reagent, but rather for its ability to alter the phenotype of the host cell in a particular detectable manner. Here, the screened library members are transformed cells, but there is a first underlying library of expression products which mediate the behavior of the cells, and a second underlying library of genes which encode those products.

Display Library

In a display library, the library members are each conjugated to, and displayed upon, a support of some kind. The support may be living (a cell or virus), or nonliving (e.g., a bead or plate).

If the support is a cell or virus, display will normally be effectuated by expressing a fusion protein which comprises the library member, a carrier moiety allowing integration of the fusion protein into the surface of the cell or virus, and optionally a lining moiety. In a variation on this theme, the cell coexpresses a first fusion comprising the library member and a linking moiety L1, and a second fusion comprising a linking moiety L2 and the carrier moiety. L1 and L2 interact to associate the first fusion with the second fusion and hence, indirectly, the library member with the surface of the cell or virus.

Soluble Library

In a soluble library, the library members are free in solution. A soluble library may be produced directly, or one may first make a display library and then release the library members from their supports.

Encapsulated Library

In an encapsulated library, the library members are inside cells or liposomes. Generally speaking, encapsulated libraries are used to store the library members for future use; the members are extracted in some way for screening purposes. However, if they differentially affect the phenotype of the cells, they may be screened indirectly by screening the cells.

cDNA Library

A cDNA library is usually prepared by extracting RNA from cells of particular origin, fractionating the RNA to isolate the messenger RNA (mRNA has a poly(A) tail, so this is usually done by oligo-dT affinity chromatography), synthesizing complementary DNA (cDNA) using reverse transcriptase, DNA polymerase, and other enzymes, subcloning the cDNA into vectors, and introducing the vectors into cells. Often, only mRNAs or cDNAs of particular sizes will be used, to make it more likely that the cDNA encodes a functional polypeptide.

A cDNA library explores the natural diversity of the transcribed DNAs of cells from a particular source. It is not a combinatorial library.

A cDNA library may be used to make a hybridization library, or it may be used as an (or to make) expression library.

Genomic DNA Library

A genomic DNA library is made by extracting DNA from a particular source, fragmenting the DNA, isolating fragments of a particular size range, subcloning the DNA fragments into vectors, and introducing the vectors into cells.

Like a cDNA library, a genomic DNA library is a natural diversity library, and not a combinatorial library. A genomic DNA library may be used the same way as a cDNA library.

Synthetic DNA library

A synthetic DNA library may be screened directly (as a hybridization library), or used in the creation of an expression or display library of peptides/proteins.

Combinatorial Libraries

The term "combinatorial library" refers to a library in which the individual members are either systematic or random combinations of a limited set of basic elements, the properties of each member being dependent on the choice and location of the elements incorporated into it. Typically, the members of the library are at least capable of being screened simultaneously. Randomization may be complete or partial; some positions may be randomized and others predetermined, and at random positions, the choices may be limited in a predetermined manner. The members of a combinatorial library may be oligomers or polymers of some kind, in which the variation occurs through the choice of monomeric building block at one or more positions of the oligomer or polymer, and possibly in terms of the connecting linkage, or the length of the oligomer or polymer, too. Or the members may be nonoligomeric molecules with a standard core structure, like the 1,4-benzodiazepine structure, with the variation being introduced by the choice of substituents at particular variable sites on the core structure. Or the members may be nonoligomeric molecules assembled like a jigsaw puzzle, but wherein each piece has both one or more variable moieties (contributing to library diversity) and one or more constant moieties (providing the functionalities for coupling the piece in question to other pieces).

Thus, in a typical combinatorial library, chemical building blocks are at least partially randomly combined into a large number (as high as 10^{15}) of different compounds,

which are then simultaneously screened for binding (or other) activity against one or more targets.

In a "simple combinatorial library", all of the members belong to the same class of compounds (e.g., peptides) and can be synthesized simultaneously. A "composite combinatorial library" is a mixture of two or more simple libraries, e.g., DNAs and peptides, or peptides, peptoids, and PNAs, or benzodiazepines and carbamates. The number of component simple libraries in a composite library will, of course, normally be smaller than the average number of members in each simple library, as otherwise the advantage of a library over individual synthesis is small.

Libraries of thousands, even millions, of random oligopeptides have been prepared by chemical synthesis (Houghten et al., *Nature*, 354:84-6(1991)), or gene expression (Marks et al., *J Mol Biol*, 222:581-97(1991)), displayed on chromatographic supports (Lam et al., *Nature*, 354:82-4(1991)), inside bacterial cells (Colas et al., *Nature*, 380:548-550(1996)), on bacterial pili (Lu, *Bio/Technology*, 13:366-372(1990)), or phage (Smith, *Science*, 228:1315-7(1985)), and screened for binding to a variety of targets including antibodies (Valadon et al., *J Mol Biol*, 261:11-22(1996)), cellular proteins (Schmitz et al., *J Mol Biol*, 260:664-677(1996)), viral proteins (Hong and Boulanger, *Embo J*, 14:4714-4727(1995)), bacterial proteins (Jacobsson and Frykberg, *Biotechniques*, 18:878-885(1995)), nucleic acids (Cheng et al., *Gene*, 171:1-8(1996)), and plastic (Siani et al., *J Chem Inf Comput Sci*, 34:588-593(1994)).

Libraries of proteins (Ladner, USP 4,664,989), peptoids (Simon et al., *Proc Natl Acad Sci U S A*, 89:9367-71(1992)), nucleic acids (Ellington and Szostak, *Nature*, 246:818(1990)), carbohydrates, and small organic molecules (Eichler et al., *Med Res Rev*, 15:481-96(1995)) have also been prepared or suggested for drug screening purposes.

The first combinatorial libraries were composed of peptides or proteins, in which all or selected amino acid positions were randomized. Peptides and proteins can exhibit high and specific binding activity, and can act as catalysts. In consequence, they are of great importance in biological systems.

Nucleic acids have also been used in combinatorial libraries. Their great advantage is the ease with which a nucleic acid with appropriate binding activity can be amplified. As a result, combinatorial libraries composed of nucleic acids can be of low redundancy and hence, of high diversity.

There has also been much interest in combinatorial libraries based on small molecules, which are more suited to pharmaceutical use, especially those which, like benzodiazepines, belong to a chemical class which has already yielded useful pharmacological agents. The techniques of combinatorial chemistry have been recognized as the most efficient means for finding small molecules that act on these targets. At present, small molecule combinatorial chemistry involves the synthesis of either pooled or discrete molecules that present varying arrays of functionality on a common scaffold. These compounds are grouped in libraries that are then screened against the target of interest either for binding or for inhibition of biological activity.

The size of a library is the number of molecules in it. The simple diversity of a library is the number of unique structures in it. There is no formal minimum or maximum diversity. If the library has a very low diversity, the library has little advantage over just synthesizing and screening the members individually. If the library is of very high diversity, it may be inconvenient to handle, at least without automatizing the process. The simple diversity of a library is preferably at least 10^1 , 10^2 , 10^3 , 10^4 , 10^6 , 10^7 , 10^8 or 10^9 , the higher the better under most circumstances. The simple diversity is usually not more than 10^{15} , and more usually not more than 10^{10} .

The average sampling level is the size divided by the simple diversity. The expected average sampling level must be high enough to provide a reasonable assurance that, if a given structure were expected, as a consequence of the library design, to be present, that the actual average sampling level will be high enough so that the structure, if satisfying the screening criteria, will yield a positive result when the library is screened. Thus, the preferred average sampling level is a function of the detection limit, which in turn is a function of the strength of the signal to be screened.

There are more complex measures of diversity than simple diversity. These attempt to take into account the degree of structural difference between the various unique sequences. These more complex measures are usually used in the context of small organic compound libraries, see below.

The library members may be presented as solutes in solution, or immobilized on some form of support. In the latter case, the support may be living (cell, virus) or nonliving (bead, plate, etc.). The supports may be separable (cells, virus particles, beads) so that binding and nonbinding members can be separated, or nonseparable (plate). In the latter case, the members will normally be placed on addressable positions on the support. The advantage of a soluble library is that there is no carrier moiety that could interfere with the binding of the members to the support. The advantage of an immobilized library is that it is easier to identify the structure of the members which were positive.

When screening a soluble library, or one with a separable support, the target is usually immobilized. When screening a library on a nonseparable support, the target will usually be labeled.

Oligonucleotide Libraries

An oligonucleotide library is a combinatorial library, at least some of whose members are single-stranded oligonucleotides having three or more nucleotides connected by phosphodiester or analogous bonds. The oligonucleotides may be linear, cyclic or branched, and may include non-nucleic acid moieties. The nucleotides are not limited to the nucleotides normally found in DNA or RNA. For examples of nucleotides modified to increase nuclease resistance and chemical stability of aptamers, see Chart 1 in Osborne and Ellington, Chem. Rev., 97: 349-70 (1997). For screening of RNA, see Ellington and Szostak, Nature, 346: 818-22 (1990).

There is no formal minimum or maximum size for these oligonucleotides. However, the number of conformations which an oligonucleotide can assume increases exponentially with its length in bases. Hence, a longer oligonucleotide is more likely to be able to fold to adapt itself to a protein surface. On the other hand, while very long molecules can be synthesized and screened, unless they provide a much superior affinity to that of shorter molecules, they are not likely to be found in the selected population, for the reasons explained by Osborne and Ellington (1997). Hence, the libraries of the present invention are preferably composed of oligonucleotides having a length of 3 to 100 bases, more preferably 15 to 35 bases. The oligonucleotides in a given library may be of the same or of different lengths.

Oligonucleotide libraries have the advantage that libraries of very high diversity (e.g., 10^{15}) are feasible, and binding molecules are readily amplified in vitro by polymerase chain reaction (PCR). Moreover, nucleic acid molecules can have very high specificity and affinity to targets.

In a preferred embodiment, this invention prepares and screens oligonucleotide libraries by the SELEX method, as described in King and Famulok, *Molec. Biol. Repts.*, 20: 97-107 (1994); L. Gold, C. Tuerk. *Methods of producing nucleic acid ligands*, US#5595877; Oliphant et al. *Gene* 44:177 (1986).

The term "aptamer" is conferred on those oligonucleotides which bind the target protein. Such aptamers may be used to characterize the target protein, both directly (through identification of the aptamer and the points of contact between the aptamer and the protein) and

indirectly (by use of the aptamer as a ligand to modify the chemical reactivity of the protein).

In a classic oligonucleotide, each nucleotide (monomeric unit) is composed of a phosphate group, a sugar moiety, and either a purine or a pyrimidine base. In DNA, the sugar is deoxyribose and in RNA it is ribose. The nucleotides are linked by 5'-3' phosphodiester bonds.

The deoxyribose phosphate backbone of DNA can be modified to increase resistance to nuclease and to increase penetration of cell membranes. Derivatives such as mono- or dithiophosphates, methyl phosphonates, boranophosphates, formacetals, carbamates, siloxanes, and dimethylenethio- -sulfoxideo- and-sulfono- linked species are known in the art.

Peptide Library

A peptide is composed of a plurality of amino acid residues joined together by peptidyl (-NHCO-) bonds. A biogenic peptide is a peptide in which the residues are all genetically encoded amino acid residues; it is not necessary that the biogenic peptide actually be produced by gene expression.

Amino acids are the basic building blocks with which peptides and proteins are constructed. Amino acids possess both an amino group (-NH₂) and a carboxylic acid group (-COOH). Many amino acids, but not all, have the alpha amino acid structure NH₂-CHR-COOH, where R is hydrogen, or any of a variety of functional groups.

Twenty amino acids are genetically encoded: Alanine, Arginine, Asparagine, Aspartic Acid, Cysteine, Glutamic Acid, Glutamine, Glycine, Histidine, Isoleucine, Leucine, Lysine, Methionine, Phenylalanine, Proline, Serine, Threonine, Tryptophan, Tyrosine, and Valine. Of these, all

save Glycine are optically isomeric, however, only the L-form is found in humans. Nevertheless, the D-forms of these amino acids do have biological significance; D-Phe, for example, is a known analgesic.

Many other amino acids are also known, including: 2-Aminoadipic acid; 3-Aminoadipic acid; beta-Aminopropionic acid; 2-Aminobutyric acid; 4-Aminobutyric acid (Piperidinic acid); 6-Aminocaproic acid; 2-Aminoheptanoic acid; 2-Aminoisobutyric acid, 3-Aminoisobutyric acid; 2-Aminopimelic acid; 2,4-Diaminobutyric acid; Desmosine; 2,2'-Diaminopimelic acid; 2,3-Diaminopropionic acid; N-Ethylglycine; N-Ethylasparagine; Hydroxylysine; allo-Hydroxylysine; 3-Hydroxyproline; 4-Hydroxyproline; Isodesmosine; allo-Isoleucine; N-Methylglycine (Sarcosine); N-Methylisoleucine; N-Methylvaline; Norvaline; Norleucine; and Ornithine.

Peptides are constructed by condensation of amino acids and/or smaller peptides. The amino group of one amino acid (or peptide) reacts with the carboxylic acid group of a second amino acid (or peptide) to form a peptide (-NHCO-) bond, releasing one molecule of water. Therefore, when an amino acid is incorporated into a peptide, it should, technically speaking, be referred to as an amino acid residue. The core of that residue is the moiety which excludes the -NH and -CO linking functionalities which connect it to other residues. This moiety consists of one or more main chain atoms (see below) and the attached side chains.

The main chain moiety of each amino acid consists of the -NH and -CO linking functionalities and a core main chain moiety. Usually the latter is a single carbon atom. However, the core main chain moiety may include additional carbon atoms, and may also include nitrogen, oxygen or sulfur atoms, which together form a single chain. In a

preferred embodiment, the core main chain atoms consist solely of carbon atoms.

The side chains are attached to the core main chain atoms. For alpha amino acids, in which the side chain is attached to the alpha carbon, the C-1, C-2 and N-2 of each residue form the repeating unit of the main chain, and the word "side chain" refers to the C-3 and higher numbered carbon atoms and their substituents. It also includes H atoms attached to the main chain atoms.

Amino acids may be classified according to the number of carbon atoms which appear in the main chain between the carbonyl carbon and amino nitrogen atoms which participate in the peptide bonds. Among the 150 or so amino acids which occur in nature, alpha, beta, gamma and delta amino acids are known. These have 1-4 intermediary carbons. Only alpha amino acids occur in proteins. Proline is a special case of an alpha amino acid; its side chain also binds to the peptide bond nitrogen.

For beta and higher order amino acids, there is a choice as to which main chain core carbon a side chain other than H is attached to. The preferred attachment site is the C-2 (alpha) carbon, i.e., the one adjacent to the carboxyl carbon of the -CO linking functionality. It is also possible for more than one main chain atom to carry a side chain other than H. However, in a preferred embodiment, only one main chain core atom carries a side chain other than H.

A main chain carbon atom may carry either one or two side chains; one is more common. A side chain may be attached to a main chain carbon atom by a single or a double bond; the former is more common.

A simple combinatorial peptide library is one whose members are peptides having three or more amino acids connected via peptide bonds.

The peptides may be linear, branched, or cyclic, and may covalently or noncovalently include nonpeptidyl moieties. The amino acids are not limited to the naturally occurring or to the genetically encoded amino acids.

A biased peptide library is one in which one or more (but not all) residues of the peptides are constant residues.

Cyclic Peptides

Many naturally occurring peptides are cyclic. Cyclization is a common mechanism for stabilization of peptide conformation thereby achieving improved association of the peptide with its ligand and hence improved biological activity. Cyclization is usually achieved by intra-chain cystine formation, by formation of peptide bond between side chains or between N- and C- terminals. Cyclization was usually achieved by peptides in solution, but several publications have appeared that describe cyclization of peptides on beads.

A peptide library may be an oligopeptide library or a protein library.

Oligopeptides

Preferably, the oligopeptides are at least five, six, seven or eight amino acids in length. Preferably, they are composed of less than 50, more preferably less than 20 amino acids.

In the case of an oligopeptide library, all or just some of the residues may be variable. The oligopeptide may be unconstrained, or constrained to a particular conformation by, e.g., the participation of constant cysteine residues in the formation of a constraining disulfide bond.

Proteins

Proteins, like oligopeptides, are composed of a plurality of amino acids, but the term protein is usually reserved for longer peptides, which are able to fold into a stable conformation. A protein may be composed of two or more polypeptide chains, held together by covalent or noncovalent crosslinks. These may occur in a homooligomeric or a heterooligomeric state.

A peptide is considered a protein if it (1) is at least 50 amino acids long, or (2) has at least two stabilizing covalent crosslinks (e.g., disulfide bonds). Thus, conotoxins are considered proteins.

Usually, the proteins of a protein library will be characterizable as having both constant residues (the same for all proteins in the library) and variable residues (which vary from member to member). This is simply because, for a given range of variation at each position, the sequence space (simple diversity) grows exponentially with the number of residue positions, so at some point it becomes inconvenient for all residues of a peptide to be variable positions. Since proteins are usually larger than oligopeptides, it is more common for protein libraries than oligopeptide libraries to feature variable positions.

In the case of a protein library, it is desirable to focus the mutations at those sites which are tolerant of mutation. These may be determined by alanine scanning mutagenesis or by comparison of the protein sequence to that of homologous proteins of similar activity. It is also more likely that mutation of surface residues will directly affect binding. Surface residues may be determined by inspecting a 3D structure of the protein, or by labeling the

surface and then ascertaining which residues have received labels. They may also be inferred by identifying regions of high hydrophilicity within the protein.

Because proteins are often altered at some sites but not others, protein libraries can be considered a special case of the biased peptide library.

There are several reasons that one might screen a protein library instead of an oligopeptide library, including (1) a particular protein, mutated in the library, has the desired activity to some degree already, and (2) the oligopeptides are not expected to have a sufficiently high affinity or specificity since they do not have a stable conformation.

When the protein library is based on a parental protein which does not have the desired activity, the parental protein will usually be one which is of high stability (melting point ≥ 50 deg. C.) and/or possessed of hypervariable regions.

The variable domains of an antibody possess hypervariable regions and hence, in some embodiments, the protein library comprises members which comprise a mutant of VH or VL chain, or a mutant of an antigen-specific binding fragment of such a chain. VH and VL chains are usually each about 110 amino acid residues, and are held in proximity by a disulfide bond between the adjoining CL and CH1 regions to form a variable domain. Together, the VH, VL, CL and CH1 form an Fab fragment.

In human heavy chains, the hypervariable regions are at 31-35, 49-65, 98-111 and 84-88, but only the first three are involved in antigen binding. There is variation among VH and VL chains at residues outside the hypervariable regions, but to a much lesser degree.

A sequence is considered a mutant of a VH or VL chain if it is at least 80% identical to a naturally occurring VH or VL chain at all residues outside the hypervariable region.

In a preferred embodiment, such antibody library members comprise both at least one VH chain and at least one VL chain, at least one of which is a mutant chain, and which chains may be derived from the same or different antibodies. The VH and VL chains may be covalently joined by a suitable linker moiety, as in a "single chain antibody", or they may be noncovalently joined, as in a naturally occurring variable domain.

If the joining is noncovalent, and the library is displayed on cells or virus, then either the VH or the VL chain may be fused to the carrier surface/coat protein. The complementary chain may be co-expressed, or added exogenously to the library.

The members may further comprise some or all of an antibody constant heavy and/or constant light chain, or a mutant thereof.

Peptoid Library

A peptoid is an analogue of a peptide in which one or more of the peptide bonds (-NH-CO-) are replaced by pseudopeptide bonds, which may be the same or different. It is not necessary that all of the peptide bonds be replaced, i.e., a peptoid may include one or more conventional amino acid residues, e.g., proline.

A peptide bond has two small divalent linker elements, -NH- and -CO-. Thus, a preferred class of pseudopeptide bonds are those which consist of two small divalent linker elements. Each may be chosen independently from the group consisting of amine (-NH-), substituted amine (-NR-), carbonyl (-CO-), thiocarbonyl (-CS-), methylene (-CH₂-),

monosubstituted methylene (-CHR-), disubstituted methylene (-CR₁R₂-), ether (-O-) and thioether (-S-). The more preferred pseudopeptide bonds include:

N-modified -NRCO-

Carba Ψ -CH₂-CH₂-

Depsi Ψ -CO-O-

Hydroxyethylene Ψ -CHOH-CH₂-

Ketomethylene Ψ -CO-CH₂-

Methylene-Oxy -CH₂-O-

Reduced -CH₂-NH-

Thiomethylene -CH₂-S-

Thiopeptide -CS-NH-

Retro-Inverso -CO-NH-

A single peptoid molecule may include more than one kind of pseudopeptide bond.

For the purposes of introducing diversity into a peptoid library, one may vary (1) the side chains attached to the core main chain atoms of the monomers linked by the pseudopeptide bonds, and/or (2) the side chains (e.g., the -R of an -NRCO-) of the pseudopeptide bonds. Thus, in one embodiment, the monomeric units which are not amino acid residues are of the structure -NR₁-CR₂-CO-, where at least one of R₁ and R₂ are not hydrogen. If there is variability in the pseudopeptide bond, this is most conveniently done by using an -NRCO- or other pseudopeptide bond with an R group, and varying the R group. In this event, the R group will usually be any of the side chains characterizing the amino acids of peptides, as previously discussed.

If the R group of the pseudopeptide bond is not variable, it will usually be small, e.g., not more than 10 atoms (e.g., hydroxyl, amino, carboxyl, methyl, ethyl, propyl).

If the conjugation chemistries are compatible, a simple combinatorial library may include both peptides and peptoids.

Peptide Nucleic Acid Library

A PNA oligomer is here defined as one comprising a plurality of units, at least one of which is a PNA monomer which comprises a side chain comprising a nucleobase. For nucleobases, see USP 6,077,835.

The classic PNA oligomer is composed of (2-aminoethyl)glycine units, with nucleobases attached by methylene carbonyl linkers. That is, it has the structure



where the outer parenthesized substructure is the PNA monomer.

In this structure, the nucleobase B is separated from the backbone N by three bonds, and the points of attachment of the side chains are separated by six bonds. The nucleobase may be any of the bases included in the nucleotides discussed in connection with oligonucleotide libraries. The bases of nucleotides A, G, T, C and U are preferred.

A PNA oligomer may further comprise one or more amino acid residues, especially glycine and proline.

One can readily envision related molecules in which (1) the -COCH₂- linker is replaced by another linker, especially one composed of two small divalent linkers as defined previously, (2) a side chain is attached to one of the three main chain carbons not participating in the peptide bond (either instead or in addition to the side chain attached to

the N of the classic PNA); and/or (3) the peptide bonds are replaced by pseudopeptide bonds as disclosed previously in the context of peptoids.

PNA oligomer libraries have been made; see e.g. Cook, 6,204,326.

Small Organic Compound Library

The small organic compound library ("compound library", for short) is a combinatorial library whose members are suitable for use as drugs if, indeed, they have the ability to mediate a biological activity of the target protein.

Peptides have certain disadvantages as drugs. These include susceptibility to degradation by serum proteases, and difficulty in penetrating cell membranes. Preferably, all or most of the compounds of the compound library avoid, or at least do not suffer to the same degree, one or more of the pharmaceutical disadvantages of peptides.

In designing a compound library, it is helpful to bear in mind the methods of molecular modification typically used to obtain new drugs. Three basic kinds of modification may be identified: disjunction, in which a lead drug is simplified to identify its component pharmacophoric moieties; conjunction, in which two or more known pharmacophoric moieties, which may be the same or different, are associated, covalently or noncovalently, to form a new drug; and alteration, in which one moiety is replaced by another which may be similar or different, but which is not in effect a disjunction or conjunction. The use of the terms "disjunction", "conjunction" and "alteration" is intended only to connote the structural relationship of the end product to the original leads, and not how the new drugs are actually synthesized, although it is possible that the two are the same.

The process of disjunction is illustrated by the evolution of neostigmine (1931) and edrophonium (1952) from physostigmine (1925). Subsequent conjunction is illustrated by demecarium (1956) and ambenonium (1956).

Alterations may modify the size, polarity, or electron distribution of an original moiety. Alterations include ring closing or opening, formation of lower or higher homologues, introduction or saturation of double bonds, introduction of optically active centers, introduction, removal or replacement of bulky groups, isosteric or bioisosteric substitution, changes in the position or orientation of a group, introduction of alkylating groups, and introduction, removal or replacement of groups with a view toward inhibiting or promoting inductive (electrostatic) or conjugative (resonance) effects.

Thus, the substituents may include electron acceptors and/or electron donors. Typical electron donors (+I) include $-\text{CH}_3$, $-\text{CH}_2\text{R}$, $-\text{CHR}_2$, $-\text{CR}_3$ and $-\text{COO}^-$. Typical electron acceptors (-I) include $-\text{NH}_3^+$, $-\text{NR}_3^+$, $-\text{NO}_2$, $-\text{CN}$, $-\text{COOH}$, $-\text{COOR}$, $-\text{CHO}$, $-\text{COR}$, $-\text{COR}$, $-\text{F}$, $-\text{Cl}$, $-\text{Br}$, $-\text{OH}$, $-\text{OR}$, $-\text{SH}$, $-\text{SR}$, $-\text{CH}=\text{CH}_2$, $-\text{CR}=\text{CR}_2$, and $-\text{C}=\text{CH}$.

The substituents may also include those which increase or decrease electronic density in conjugated systems. The former (+R) groups include $-\text{CH}_3$, $-\text{CR}_3$, $-\text{F}$, $-\text{Cl}$, $-\text{Br}$, $-\text{I}$, $-\text{OH}$, $-\text{OR}$, $-\text{OCOR}$, $-\text{SH}$, $-\text{SR}$, $-\text{NH}_2$, $-\text{NR}_2$, and $-\text{NHCOR}$. The later (-R) groups include $-\text{NO}_2$, $-\text{CN}$, $-\text{CHC}$, $-\text{COR}$, $-\text{COOH}$, $-\text{COOR}$, $-\text{CONH}_2$, $-\text{SO}_2\text{R}$ and $-\text{CF}_3$.

Synthetically speaking, the modifications may be achieved by a variety of unit processes, including nucleophilic and electrophilic substitution, reduction and oxidation, addition elimination, double bond cleavage, and cyclization.

For the purpose of constructing a library, a compound, or a family of compounds, having one or more pharmacological

activities (which need not be related to the known or suspected activities of the target protein), may be disjoined into two or more known or potential pharmacophoric moieties. Analogues of each of these moieties may be identified, and mixtures of these analogues reacted so as to reassemble compounds which have some similarity to the original lead compound. It is not necessary that all members of the library possess moieties analogous to all of the moieties of the lead compound.

The design of a library may be illustrated by the example of the benzodiazepines. Several benzodiazepine drugs, including chlordiazepoxide, diazepam and oxazepam, have been used as anti-anxiety drugs. Derivatives of benzodiazepines have widespread biological activities; derivatives have been reported to act not only as anxiolytics, but also as anticonvulsants; cholecystokinin (CCK) receptor subtype A or B, kappa opioid receptor, platelet activating factor, and HIV transactivator Tat antagonists, and GPIIbIIIa, reverse transcriptase and ras farnesyltransferase inhibitors.

The benzodiazepine structure has been disjoined into a 2-aminobenzophenone, an amino acid, and an alkylating agent. See Bunin, et al., Proc. Nat. Acad. Sci. USA, 91:4708 (1994). Since only a few 2-aminobenzophenone derivatives are commercially available, it was later disjoined into 2-aminoarylstannane, an acid chloride, an amino acid, and an alkylating agent. Bunin, et al., Meth. Enzymol., 267:448 (1996). The arylstannane may be considered the core structure upon which the other moieties are substituted, or all four may be considered equals which are conjoined to make each library member.

A basic library synthesis plan and member structure is shown in Figure 1 of Fowlkes, et al., U.S. Serial No. 08/740,671, incorporated by reference in its entirety. The

acid chloride building block introduces variability at the R¹ site. The R² site is introduced by the amino acid, and the R³ site by the alkylating agent. The R⁴ site is inherent in the arylstannane. Bunin, et al. generated a 1, 4-benzodiazepine library of 11,200 different derivatives prepared from 20 acid chlorides, 35 amino acids, and 16 alkylating agents. (No diversity was introduced at R⁴; this group was used to couple the molecule to a solid phase.) According to the Available Chemicals Directory (HDL Information Systems, San Leandro CA), over 300 acid chlorides, 80 Fmoc-protected amino acids and 800 alkylating agents were available for purchase (and more, of course, could be synthesized). The particular moieties used were chosen to maximize structural dispersion, while limiting the numbers to those conveniently synthesized in the wells of a microtiter plate. In choosing between structurally similar compounds, preference was given to the least substituted compound.

The variable elements included both aliphatic and aromatic groups. Among the aliphatic groups, both acyclic and cyclic (mono- or poly-) structures, substituted or not, were tested. (While all of the acyclic groups were linear, it would have been feasible to introduce a branched aliphatic). The aromatic groups featured either single and multiple rings, fused or not, substituted or not, and with heteroatoms or not. The secondary substituents included -NH₂, -OH, -OMe, -CN, -Cl, -F, and -COOH. While not used, spacer moieties, such as -O-, -S-, -OO-, -CS-, -NH-, and -NR-, could have been incorporated.

Bunin et al. suggest that instead of using a 1, 4-benzodiazepine as a core structure, one may instead use a 1, 4-benzodiazepine-2, 5-dione structure.

As noted by Bunin et al., it is advantageous, although not necessary, to use a linkage strategy which leaves no

trace of the linking functionality, as this permits construction of a more diverse library.

Other combinatorial nonoligomeric compound libraries known or suggested in the art have been based on carbamates, mercaptoacylated pyrrolidines, phenolic agents, aminimides, N-acylamino ethers (made from amino alcohols, aromatic hydroxy acids, and carboxylic acids), N-alkylamino ethers (made from aromatic hydroxy acids, amino alcohols and aldehydes) 1, 4-piperazines, and 1, 4-piperazine-6-ones.

DeWitt, et al., Proc. Nat. Acad. Sci. (USA), 90:6909-13 (1993) describe the simultaneous but separate, synthesis of 40 discrete hydantoins and 40 discrete benzodiazepines. They carry out their synthesis on a solid support (inside a gas dispersion tube), in an array format, as opposed to other conventional simultaneous synthesis techniques (e.g., in a well, or on a pin). The hydantoins were synthesized by first simultaneously deprotecting and then treating each of five amino acid resins with each of eight isocyanates. The benzodiazepines were synthesized by treating each of five deprotected amino acid resins with each of eight 2-amino benzophenone imines.

Chen, et al., J. Am. Chem. Soc., 116:2661-62 (1994) described the preparation of a pilot (9 member) combinatorial library of formate esters. A polymer bead-bound aldehyde preparation was "split" into three aliquots, each reacted with one of three different ylide reagents. The reaction products were combined, and then divided into three new aliquots, each of which was reacted with a different Michael donor. Compound identity was found to be determinable on a single bead basis by gas chromatography/mass spectroscopy analysis.

Holmes, USP 5,549,974 (1996) sets forth methodologies for the combinatorial synthesis of libraries of thiazolidinones and metathiazanones. These libraries are

made by combination of amines, carbonyl compounds, and thiols under cyclization conditions.

Ellman, USP 5,545,568 (1996) describes combinatorial synthesis of benzodiazepines, prostaglandins, beta-turn mimetics, and glycerol-based compounds. See also Ellman, USP 5,288,514.

Summerton, USP 5,506,337 (1996) discloses methods of preparing a combinatorial library formed predominantly of morpholino subunit structures.

Heterocyclic combinatorial libraries are reviewed generally in Nefzi, et al., Chem. Rev., 97:449-472 (1997).

For pharmacological classes, see, e.g., Goth, Medical Pharmacology: Principles and Concepts (C.V. Mosby Co.: 8th ed. 1976); Korolkovas and Burckhalter, Essentials of Medicinal Chemistry (John Wiley & Sons, Inc.: 1976). For synthetic methods, see, e.g., Warren, Organic Synthesis: The Disconnection Approach (John Wiley & Sons, Ltd.: 1982); Fuson, Reactions of Organic Compounds (John Wiley & Sons: 1966); Payne and Payne, How to do an Organic Synthesis (Allyn and Bacon, Inc.: 1969); Greene, Protective Groups in Organic Synthesis (Wiley-Interscience). For selection of substituents, see e.g., Hansch and Leo, Substituent Constants for Correlation Analysis in Chemistry and Biology (John Wiley & Sons: 1979).

The library is preferably synthesized so that the individual members remain identifiable so that, if a member is shown to be active, it is not necessary to analyze it. Several methods of identification have been proposed, including:

- (1) encoding, i.e., the attachment to each member of an identifier moiety which is more readily identified than the member proper. This has the

disadvantage that the tag may itself influence the activity of the conjugate.

- (2) spatial addressing, e.g., each member is synthesized only at a particular coordinate on or in a matrix, or in a particular chamber. This might be, for example, the location of a particular pin, or a particular well on a microtiter plate, or inside a "tea bag".

The present invention is not limited to any particular form of identification.

However, it is possible to simply characterize those members of the library which are found to be active, based on the characteristic spectroscopic indicia of the various building blocks.

Solid phase synthesis permits greater control over which derivatives are formed. However, the solid phase could interfere with activity. To overcome this problem, some or all of the molecules of each member could be liberated, after synthesis but before screening.

Examples of candidate simple libraries which might be evaluated include derivatives of the following:

Cyclic Compounds Containing One Hetero Atom

Heteronitrogen

pyrroles

pentasubstituted pyrroles

pyrrolidines

pyrrolines

prolines

indoles

beta-carbolines

pyridines

dihydropyridines

1,4-dihydropyridines

119

pyrido[2,3-d]pyrimidines

tetrahydro-3H-imidazo[4,5-c] pyridines

Isoquinolines

tetrahydroisoquinolines

quinolones

beta-lactams

azabicyclo[4.3.0]nonen-8-one amino acid

Heterooxygen

furans

tetrahydrofurans

2,5-disubstituted tetrahydrofurans

pyrans

hydroxypyranones

tetrahydroxypyranones

gamma-butyrolactones

Heterosulfur

sulfolenes

Cyclic Compounds with Two or More Hetero atoms

Multiple heteronitrogens

imidazoles

pyrazoles

piperazines

diketopiperazines

arylpiperazines

benzylpiperazines

benzodiazepines

1,4-benzodiazepine-2,5-diones

hydantoins

5-alkoxyhydantoins

dihydropyrimidines

1,3-disubstituted-5,6-dihydropyrimidine-2,4-diones

120

cyclic ureas

cyclic thioureas

quinazolines

chiral 3-substituted-quinazoline-2,4-

diones

triazoles

1,2,3-triazoles

purines

Heteronitrogen and Heterooxygen

dikelomorpholines

isoxazoles

isoxazolines

Heteronitrogen and Heterosulfur

thiazolidines

N-axylthiazolidines

dihydrothiazoles

2-methylene-2,3-dihydrothiazates

2-aminothiazoles

thiophenes

3-amino thiophenes

4-thiazolidinones

4-melathiazanones

benzisothiazolones

For details on synthesis of libraries, see Nefzi, et al., Chem. Rev., 97:449-72 (1997), and references cited therein.

Pharmaceutical Methods and Preparations

The preferred animal subject of the present invention is a mammal. By the term "mammal" is meant an individual belonging to the class Mammalia. The invention is particularly useful in the treatment of human subjects, although it is intended for veterinary and nutritional uses

as well. Preferred nonhuman subjects are of the orders Primata (e.g., apes and monkeys), Artiodactyla or Perissodactyla (e.g., cows, pigs, sheep, horses, goats), Carnivora (e.g., cats, dogs), Rodenta (e.g., rats, mice, guinea pigs, hamsters), Lagomorpha (e.g., rabbits) or other pet, farm or laboratory mammals.

The term "protection", as used herein, is intended to include "prevention," "suppression" and "treatment." "Prevention", strictly speaking, involves administration of the pharmaceutical prior to the induction of the disease (or other adverse clinical condition). "Suppression" involves administration of the composition prior to the clinical appearance of the disease. "Treatment" involves administration of the protective composition after the appearance of the disease.

It will be understood that in human and veterinary medicine, it is not always possible to distinguish between "preventing" and "suppressing" since the ultimate inductive event or events may be unknown, latent, or the patient is not ascertained until well after the occurrence of the event or events. Therefore, unless qualified, the term "prevention" will be understood to refer to both prevention in the strict sense, and to suppression.

The preventative or prophylactic use of a pharmaceutical usually involves identifying subjects who are at higher risk than the general population of contracting the disease, and administering the pharmaceutical to them in advance of the clinical appearance of the disease. The effectiveness of such use is measured by comparing the subsequent incidence or severity of the disease, or of particular symptoms of the disease, in the treated subjects against that in untreated subjects of the same high risk group.

While high risk factors vary from disease to disease, in general, these include (1) prior occurrence of the disease in one or more members of the same family, or, in the case of a contagious disease, in individuals with whom the subject has come into potentially contagious contact at a time when the earlier victim was likely to be contagious, (2) a prior occurrence of the disease in the subject, (3) prior occurrence of a related disease, or a condition known to increase the likelihood of the disease, in the subject; (4) appearance of a suspicious level of a marker of the disease, or a related disease or condition; (5) a subject who is immunologically compromised, e.g., by radiation treatment, HIV infection, drug use,, etc., or (6) membership in a particular group (e.g., a particular age, sex, race, ethnic group, etc.) which has been epidemiologically associated with that disease.

In some cases, it may be desirable to provide prophylaxis for the general population, and not just a high risk group. This is most likely to be the case when essentially all are at risk of contracting the disease, the effects of the disease are serious, the therapeutic index of the prophylactic agent is high, and the cost of the agent is low.

A prophylaxis or treatment may be curative, that is, directed at the underlying cause of a disease, or ameliorative, that is, directed at the symptoms of the disease, especially those which reduce the quality of life.

It should also be understood that to be useful, the protection provided need not be absolute, provided that it is sufficient to carry clinical value. An agent which provides protection to a lesser degree than do competitive agents may still be of value if the other agents are ineffective for a particular individual, if it can be used in combination with other agents to enhance the level of

protection, or if it is safer than competitive agents. It is desirable that there be a statistically significant ($p=0.05$ or less) improvement in the treated subject relative to an appropriate untreated control, and it is desirable that this improvement be at least 10%, more preferably at least 25%, still more preferably at least 50%, even more preferably at least 100%, in some indicia of the incidence or severity of the disease or of at least one symptom of the disease.

At least one of the drugs of the present invention may be administered, by any means that achieve their intended purpose, to protect a subject against a disease or other adverse condition. The form of administration may be systemic or topical. For example, administration of such a composition may be by various parenteral routes such as subcutaneous, intravenous, intradermal, intramuscular, intraperitoneal, intranasal, transdermal, or buccal routes. Alternatively, or concurrently, administration may be by the oral route. Parenteral administration can be by bolus injection or by gradual perfusion over time.

A typical regimen comprises administration of an effective amount of the drug, administered over a period ranging from a single dose, to dosing over a period of hours, days, weeks, months, or years.

It is understood that the suitable dosage of a drug of the present invention will be dependent upon the age, sex, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect desired. However, the most preferred dosage can be tailored to the individual subject, as is understood and determinable by one of skill in the art, without undue experimentation. This will typically involve adjustment of a standard dose, e.g., reduction of the dose if the patient has a low body weight.

Prior to use in humans, a drug will first be evaluated for safety and efficacy in laboratory animals. In human clinical studies, one would begin with a dose expected to be safe in humans, based on the preclinical data for the drug in question, and on customary doses for analogous drugs (if any). If this dose is effective, the dosage may be decreased, to determine the minimum effective dose, if desired. If this dose is ineffective, it will be cautiously increased, with the patients monitored for signs of side effects. See, e.g., Berkow et al, eds., *The Merck Manual*, 15th edition, Merck and Co., Rahway, N.J., 1987; Goodman et al., eds., *Goodman and Gilman's The Pharmacological Basis of Therapeutics*, 8th edition, Pergamon Press, Inc., Elmsford, N.Y., (1990); Avery's *Drug Treatment: Principles and Practice of Clinical Pharmacology and Therapeutics*, 3rd edition, ADIS Press, LTD., Williams and Wilkins, Baltimore, MD. (1987), Ebadi, *Pharmacology*, Little, Brown and Co., Boston, (1985), which references and references cited therein, are entirely incorporated herein by reference.

The total dose required for each treatment may be administered by multiple doses or in a single dose. The protein may be administered alone or in conjunction with other therapeutics directed to the disease or directed to other symptoms thereof.

The appropriate dosage form will depend on the disease, the pharmaceutical, and the mode of administration; possibilities include tablets, capsules, lozenges, dental pastes, suppositories, inhalants, solutions, ointments and parenteral depots. See, e.g., Berker, *supra*, Goodman, *supra*, Avery, *supra* and Ebadi, *supra*, which are entirely incorporated herein by reference, including all references cited therein.

In the case of peptide drugs, the drug may be administered in the form of an expression vector comprising

a nucleic acid encoding the peptide; such a vector, after incorporation into the genetic complement of a cell of the patient, directs synthesis of the peptide. Suitable vectors include genetically engineered poxviruses (vaccinia), adenoviruses, adeno-associated viruses, herpesviruses and lentiviruses which are or have been rendered nonpathogenic.

In addition to at least one drug as described herein, a pharmaceutical composition may contain suitable pharmaceutically acceptable carriers, such as excipients, carriers and/or auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. See, e.g., Berker, *supra*, Goodman, *supra*, Avery, *supra* and Ebadi, *supra*, which are entirely incorporated herein by reference, included all references cited therein.

Assay Compositions and Methods

Target Organism

The invention contemplates that it may be appropriate to ascertain or to mediate the biological activity of a substance of this invention in a target organism.

The target organism may be a plant, animal, or microorganism.

In the case of a plant, it may be an economic plant, in which case the drug may be intended to increase the disease, weather or pest resistance, alter the growth characteristics, or otherwise improve the useful characteristics or mute undesirable characteristics of the plant. Or it may be a weed, in which case the drug may be intended to kill or otherwise inhibit the growth of the plant, or to alter its characteristics to convert it from a weed to an economic plant. The plant may be a tree, shrub, crop, grass, etc. The plant may be an algae (which are in some cases also microorganisms), or a vascular plant,

especially gymnosperms (particularly conifers) and angiosperms. Angiosperms may be monocots or dicots. The plants of greatest interest are rice, wheat, corn, alfalfa, soybeans, potatoes, peanuts, tomatoes, melons, apples, pears, plums, pineapples, fir, spruce, pine, cedar, and oak.

If the target organism is a microorganism, it may be algae, bacteria, fungi, or a virus (although the biological activity of a virus must be determined in a virus-infected cell). The microorganism may be human or other animal or plant pathogen, or it may be nonpathogenic. It may be a soil or water organism, or one which normally lives inside other living things.

If the target organism is an animal, it may be a vertebrate or a nonvertebrate animal. Nonvertebrate animals are chiefly of interest when they act as pathogens or parasites, and the drugs are intended to act as biocidal or biostatic agents. Nonvertebrate animals of interest include worms, mollusks, and arthropods.

The target organism may also be a vertebrate animal, i.e., a mammal, bird, reptile, fish or amphibian. Among mammals, the target animal preferably belongs to the order Primata (humans, apes and monkeys), Artiodactyla (e.g., cows, pigs, sheep, goats, horses), Rodenta (e.g., mice, rats) Lagomorpha (e.g., rabbits, hares), or Carnivora (e.g., cats, dogs). Among birds, the target animals are preferably of the orders Anseriformes (e.g., ducks, geese, swans) or Galliformes (e.g., quails, grouse, pheasants, turkeys and chickens). Among fish, the target animal is preferably of the order Clupeiformes (e.g., sardines, shad, anchovies, whitefish, salmon).

Target Tissues

The term "target tissue" refers to any whole animal, physiological system, whole organ, part of organ,

miscellaneous tissue, cell, or cell component (e.g., the cell membrane) of a target animal in which biological activity may be measured.

Routinely in mammals one would choose to compare and contrast the biological impact on virtually any and all tissues which express the subject receptor protein. The main tissues to use are: brain, heart, lung, kidney, liver, pancreas, skin, intestines, adipose, stomach, skeletal muscle, adrenal glands, breast, prostate, vasculature, retina, cornea, thyroid gland, parathyroid glands, thymus, bone marrow, bone, etc.

Another classification would be by cell type: B cells, T cells, macrophages, neutrophils, eosinophils, mast cells, platelets, megakaryocytes, erythrocytes, bone marrow stromal cells, fibroblasts, neurons, astrocytes, neuroglia, microglia, epithelial cells (from any organ, e.g. skin, breast, prostate, lung, intestines etc), cardiac muscle cells, smooth muscle cells, striated muscle cells, osteoblasts, osteocytes, chondroblasts, chondrocytes, keratinocytes, melanocytes, etc.

Of course, in the case of a unicellular organism, there is no distinction between the "target organism" and the "target tissue".

Screening Assays

Assays intended to determine the binding or the biological activity of a substance are called preliminary screening assays.

Screening assays will typically be either in vitro (cell-free) assays (for binding to an immobilized receptor) or cell-based assays (for alterations in the phenotype of the cell). They will not involve screening of whole multicellular organisms, or isolated organs. The comments

on diagnostic biological assays apply mutatis mutandis to screening cell-based assays.

In Vitro vs. In Vivo Assays

The term *in vivo* is descriptive of an event, such as binding or enzymatic action, which occurs within a living organism. The organism in question may, however, be genetically modified. The term *in vitro* refers to an event which occurs outside a living organism. Parts of an organism (e.g., a membrane, or an isolated biochemical) are used, together with artificial substrates and/or conditions. For the purpose of the present invention, the term *in vitro* excludes events occurring inside or on an intact cell, whether of a unicellular or multicellular organism.

In vivo assays include both cell-based assays, and organismic assays. The cell-based assays include both assays on unicellular organisms, and assays on isolated cells or cell cultures derived from multicellular organisms. The cell cultures may be mixed, provided that they are not organized into tissues or organs. The term organismic assay refers to assays on whole multicellular organisms, and assays on isolated organs or tissues of such organisms.

In vitro Diagnostic Methods and Reagents

The *in vitro* assays of the present invention may be applied to any suitable analyte-containing sample, and may be qualitative or quantitative in nature.

Sample

The sample will normally be a biological fluid, such as blood, urine, lymph, semen, milk, or cerebrospinal fluid, or a fraction or derivative thereof, or a biological tissue, in the form of, e.g., a tissue section or homogenate. However, the sample conceivably could be (or derived from) a food or

beverage, a pharmaceutical or diagnostic composition, soil, or surface or ground water. If a biological fluid or tissue, it may be taken from a human or other mammal, vertebrate or animal, or from a plant. The preferred sample is blood, or a fraction or derivative thereof.

Binding and Reaction Assays

The assay may be a binding assay, in which one step involves the binding of a diagnostic reagent to the analyte, or a reaction assay, which involves the reaction of a reagent with the analyte. The reagents used in a binding assay may be classified as to the nature of their interaction with analyte: (1) analyte analogues, or (2) analyte binding molecules (ABM). They may be labeled or insolubilized.

In a reaction assay, the assay may look for a direct reaction between the analyte and a reagent which is reactive with the analyte, or if the analyte is an enzyme or enzyme inhibitor, for a reaction catalyzed or inhibited by the analyte. The reagent may be a reactant, a catalyst, or an inhibitor for the reaction.

An assay may involve a cascade of steps in which the product of one step acts as the target for the next step. These steps may be binding steps, reaction steps, or a combination thereof.

Signal Producing System (SPS)

In order to detect the presence, or measure the amount, of an analyte, the assay must provide for a signal producing system (SPS) in which there is a detectable difference in the signal produced, depending on whether the analyte is present or absent (or, in a quantitative assay, on the amount of the analyte). The detectable signal may be one which is visually detectable, or one detectable only with

instruments. Possible signals include production of colored or luminescent products, alteration of the characteristics (including amplitude or polarization) of absorption or emission of radiation by an assay component or product, and precipitation or agglutination of a component or product. The term "signal" is intended to include the discontinuance of an existing signal, or a change in the rate of change of an observable parameter, rather than a change in its absolute value. The signal may be monitored manually or automatically.

In a reaction assay, the signal is often a product of the reaction. In a binding assay, it is normally provided by a label borne by a labeled reagent.

Labels

The component of the signal producing system which is most intimately associated with the diagnostic reagent is called the "label". A label may be, e.g., a radioisotope, a fluorophore, an enzyme, a co-enzyme, an enzyme substrate, an electron-dense compound, an agglutinable particle.

The radioactive isotope can be detected by such means as the use of a gamma counter or a scintillation counter or by autoradiography. Isotopes which are particularly useful for the purpose of the present invention include ^3H , ^{125}I , ^{131}I , ^{35}S , ^{14}C , ^{32}P and ^{33}P . ^{125}I is preferred for antibody labeling.

The label may also be a fluorophore. When the fluorescently labeled reagent is exposed to light of the proper wave length, its presence can then be detected due to fluorescence. Among the most commonly used fluorescent labelling compounds are fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthaldehyde and fluorescamine.

Alternatively, fluorescence-emitting metals such as ^{125}Eu , or others of the lanthanide series, may be incorporated into a diagnostic reagent using such metal chelating groups as diethylenetriaminepentaacetic acid (DTPA) or ethylenediamine-tetraacetic acid (EDTA).

The label may also be a chemiluminescent compound. The presence of the chemiluminescently labeled reagent is then determined by detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of particularly useful chemiluminescent labeling compounds are luminol, isolumino, thermotropic acridinium ester, imidazole, acridinium salt and oxalate ester.

Likewise, a bioluminescent compound may be used for labeling. Bioluminescence is a type of chemiluminescence found in biological systems in which a catalytic protein increases the efficiency of the chemiluminescent reaction. The presence of a bioluminescent protein is determined by detecting the presence of luminescence. Important bioluminescent compounds for purposes of labeling are luciferin, luciferase and aequorin.

Enzyme labels, such as horseradish peroxidase and alkaline phosphatase, are preferred. When an enzyme label is used, the signal producing system must also include a substrate for the enzyme. If the enzymatic reaction product is not itself detectable, the SPS will include one or more additional reactants so that a detectable product appears.

An enzyme analyte may act as its own label if an enzyme inhibitor is used as a diagnostic reagent.

Binding Assay Formats

Binding assays may be divided into two basic types, heterogeneous and homogeneous. In heterogeneous assays, the interaction between the affinity molecule and the analyte does not affect the label, hence, to determine the amount or

presence of analyte, bound label must be separated from free label. In homogeneous assays, the interaction does affect the activity of the label, and therefore analyte levels can be deduced without the need for a separation step.

In one embodiment, the ABM is insolubilized by coupling it to a macromolecular support, and analyte in the sample is allowed to compete with a known quantity of a labeled or specifically labelable analyte analogue. The "analyte analogue" is a molecule capable of competing with analyte for binding to the ABM, and the term is intended to include analyte itself. It may be labeled already, or it may be labeled subsequently by specifically binding the label to a moiety differentiating the analyte analogue from analyte. The solid and liquid phases are separated, and the labeled analyte analogue in one phase is quantified. The higher the level of analyte analogue in the solid phase, i.e., sticking to the ABM, the lower the level of analyte in the sample.

In a "sandwich assay", both an insolubilized ABM, and a labeled ABM are employed. The analyte is captured by the insolubilized ABM and is tagged by the labeled ABM, forming a ternary complex. The reagents may be added to the sample in either order, or simultaneously. The ABMs may be the same or different. The amount of labeled ABM in the ternary complex is directly proportional to the amount of analyte in the sample.

The two embodiments described above are both heterogeneous assays. However, homogeneous assays are conceivable. The key is that the label be affected by whether or not the complex is formed.

Conjugation Methods

A label may be conjugated, directly or indirectly (e.g., through a labeled anti-ABM antibody), covalently

(e.g., with SPDP) or noncovalently, to the ABM, to produce a diagnostic reagent. Similarly, the ABM may be conjugated to a solid phase support to form a solid phase ("capture") diagnostic reagent.

Suitable supports include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, agaroses, and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention.

The support material may have virtually any possible structural configuration so long as the coupled molecule is capable of binding to its target. Thus the support configuration may be spherical, as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface may be flat such as a sheet, test strip, etc.

Biological Assays

A biological assay measures or detects a biological response of a biological entity to a substance.

The biological entity may be a whole organism, an isolated organ or tissue, freshly isolated cells, an immortalized cell line, or a subcellular component (such as a membrane; this term should not be construed as including an isolated receptor). The entity may be, or may be derived from, an organism which occurs in nature, or which is modified in some way. Modifications may be genetic (including radiation and chemical mutants, and genetic engineering) or somatic (e.g., surgical, chemical, etc.). In the case of a multicellular entity, the modifications may affect some or all cells. The entity need not be the target organism, or a derivative thereof, if there is a reasonable

correlation between bioassay activity in the assay entity and biological activity in the target organism.

The entity is placed in a particular environment, which may be more or less natural. For example, a culture medium may, but need not, contain serum or serum substitutes, and it may, but need not, include a support matrix of some kind, it may be still, or agitated. It may contain particular biological or chemical agents, or have particular physical parameters (e.g., temperature), that are intended to nourish or challenge the biological entity.

There must also be a detectable biological marker for the response. At the cellular level, the most common markers are cell survival and proliferation, cell behavior (clustering, motility), cell morphology (shape, color), and biochemical activity (overall DNA synthesis, overall protein synthesis, and specific metabolic activities, such as utilization of particular nutrients, e.g., consumption of oxygen, production of CO₂, production of organic acids, uptake or discharge of ions).

The direct signal produced by the biological marker may be transformed by a signal producing system into a different signal which is more observable, for example, a fluorescent or colorimetric signal.

The entity, environment, marker and signal producing system are chosen to achieve a clinically acceptable level of sensitivity, specificity and accuracy.

In some cases, the goal will be to identify substances which mediate the biological activity of a natural biological entity, and the assay is carried out directly with that entity. In other cases, the biological entity is used simply as a model of some more complex (or otherwise inconvenient to work with) biological entity. In that event, the model biological entity is used because activity in the model system is considered more predictive of

activity in the ultimate natural biological entity than is simple binding activity in an in vitro system. The model entity is used instead of the ultimate entity because the former is more expensive or slower to work with, or because ethical considerations forbid working with the ultimate entity yet.

The model entity may be naturally occurring, if the model entity usefully models the ultimate entity under some conditions. Or it may be non-naturally occurring, with modifications that increase its resemblance to the ultimate entity.

Transgenic animals, such as transgenic mice, rats, and rabbits, have been found useful as model systems.

In cell-based model assays, where the biological activity is mediated by binding to a receptor (target protein), the receptor may be functionally connected to a signal (biological marker) producing system, which may be endogenous or exogenous to the cell.

There are a number of techniques of doing this.

"Zero-Hybrid" Systems

In these systems, the binding of a peptide to the target protein results in a screenable or selectable phenotypic change, without resort to fusing the target protein (or a ligand binding moiety thereof) to an endogenous protein. It may be that the target protein is endogenous to the host cell, or is substantially identical to an endogenous receptor so that it can take advantage of the latter's native signal transduction pathway. Or sufficient elements of the signal transduction pathway normally associated with the target protein may be engineered into the cell so that the cell signals binding to the target protein.

"One-Hybrid" Systems

In these systems, a chimera receptor, a hybrid of the target protein and an endogenous receptor, is used. The chimeric receptor has the ligand binding characteristics of the target protein and the signal transduction characteristics of the endogenous receptor. Thus, the normal signal transduction pathway of the endogenous receptor is subverted.

Preferably, the endogenous receptor is inactivated, or the conditions of the assay avoid activation of the endogenous receptor, to improve the signal-to-noise ratio.

See Fowlkes USP 5,789,184 for a yeast system.

Another type of "one-hybrid" system combines a peptide: DNA-binding domain fusion with an unfused target receptor that possesses an activation domain.

"Two-Hybrid" System

In a preferred embodiment, the cell-based assay is a two hybrid system. This term implies that the ligand is incorporated into a first hybrid protein, and the receptor into a second hybrid protein. The first hybrid also comprises component A of a signal generating system, and the second hybrid comprises component B of that system. Components A and B, by themselves, are insufficient to generate a signal. However, if the ligand binds the receptor, components A and B are brought into sufficiently close proximity so that they can cooperate to generate a signal.

Components A and B may naturally occur, or be substantially identical to moieties which naturally occur, as components of a single naturally occurring biomolecule, or they may naturally occur, or be substantially identical to moieties which naturally occur, as separate naturally occurring biomolecules which interact in nature.

Two-Hybrid System: Transcription Factor Type

In a preferred "two-hybrid" embodiment, one member of a peptide ligand:receptor binding pair is expressed as a fusion to a DNA-binding domain (DBD) from a transcription factor (this fusion protein is called the "bait"), and the other is expressed as a fusion to a transactivation domain (TAD) (this fusion protein is called the "fish", the "prey", or the "catch"). The transactivation domain should be complementary to the DNA-binding domain, i.e., it should interact with the latter so as to activate transcription of a specially designed reporter gene that carries a binding site for the DNA-binding domain. Naturally, the two fusion proteins must likewise be complementary.

This complementarity may be achieved by use of the complementary and separable DNA-binding and transcriptional activator domains of a single transcriptional activator protein, or one may use complementary domains derived from different proteins. The domains may be identical to the native domains, or mutants thereof. The assay members may be fused directly to the DBD or TAD, or fused through an intermediated linker.

The target DNA operator may be the native operator sequence, or a mutant operator. Mutations in the operator may be coordinated with mutations in the DBD and the TAD. An example of a suitable transcription activation system is one comprising the DNA-binding domain from the bacterial repressor LexA and the activation domain from the yeast transcription factor Gal4, with the reporter gene operably linked to the LexA operator.

It is not necessary to employ the intact target receptor; just the ligand-binding moiety is sufficient.

The two fusion proteins may be expressed from the same or different vectors. Likewise, the activatable reporter

gene may be expressed from the same vector as either fusion protein (or both proteins), or from a third vector.

Potential DNA-binding domains include Gal4, LexA, and mutant domains substantially identical to the above.

Potential activation domains include E. coli B42, Gal4 activation domain II, and HSV VP16, and mutant domains substantially identical to the above.

Potential operators include the native operators for the desired activation domain, and mutant domains substantially identical to the native operator.

The fusion proteins may comprise nuclear localization signals.

The assay system will include a signal producing system, too. The first element of this system is a reporter gene operably linked to an operator responsive to the DBD and TAD of choice. The expression of this reporter gene will result, directly or indirectly, in a selectable or screenable phenotype (the signal). The signal producing system may include, besides the reporter gene, additional genetic or biochemical elements which cooperate in the production of the signal. Such an element could be, for example, a selective agent in the cell growth medium. There may be more than one signal producing system, and the system may include more than one reporter gene.

The sensitivity of the system may be adjusted by, e.g., use of competitive inhibitors of any step in the activation or signal production process, increasing or decreasing the number of operators, using a stronger or weaker DBD or TAD, etc.

When the signal is the death or survival of the cell in question, or proliferation or nonproliferation of the cell in question, the assay is said to be a selection. When the signal merely results in a detectable phenotype by which the signaling cell may be differentiated from the same cell in a

nonsignaling state (either way being a living cell), the assay is a screen. However, the term "screening assay" may be used in a broader sense to include a selection. When the narrower sense is intended, we will use the term "nonselective screen".

Various screening and selection systems are discussed in Ladner, USP 5,198,346.

Screening and selection may be for or against the peptide: target protein or compound:target protein interaction.

Preferred assay cells are microbial (bacterial, yeast, algal, protozoal), invertebrate, vertebrate (esp. mammalian, particularly human). The best developed two-hybrid assays are yeast and mammalian systems.

Normally, two hybrid assays are used to determine whether a protein X and a protein Y interact, by virtue of their ability to reconstitute the interaction of the DBD and the TAD. However, augmented two-hybrid assays have been used to detect interactions that depend on a third, non-protein ligand.

For more guidance on two-hybrid assays, see Brent and Finley, Jr., *Ann. Rev. Genet.*, 31:663-704 (1997); Fremont-Racine, et al., *Nature Genetics*, 277-281 (16 July 1997); Allen, et al., *TIBS*, 511-16 (Dec. 1995); LeCrenier, et al., *BioEssays*, 20:1-6 (1998); Xu, et al., *Proc. Nat. Acad. sci. (USA)*, 94:12473-8 (Nov. 1992); Esotak, et al., *Mol. Cell. Biol.*, 15:5820-9 (1995); Yang, et al., *Nucleic Acids Res.*, 23:1152-6 (1995); Bendixen, et al., *Nucleic Acids Res.*, 22:1778-9 (1994); Fuller, et al., *BioTechniques*, 25:85-92 (July 1998); Cohen, et al., *PNAS (USA)* 95:14272-7 (1998); Kolonin and Finley, Jr., *PNAS (USA)* 95:14266-71 (1998). See also Vasavada, et al., *PNAS (USA)*, 88:10686-90 (1991) (contingent replication assay), and Rehrauer, et al., J.

Biol. Chem., 271:23865-73 91996) (LexA repressor cleavage assay).

Two-Hybrid Systems: reporter Enzyme type

In another embodiment, the components A and B reconstitute an enzyme which is not a transcription factor.

As in the last example, the effect of the reconstitution of the enzyme is a phenotypic change which may be a screenable change, a selectable change, or both.

In vivo Diagnostic Uses

Radio-labeled ABM may be administered to the human or animal subject. Administration is typically by injection, e.g., intravenous or arterial or other means of administration in a quantity sufficient to permit subsequent dynamic and/or static imaging using suitable radio-detecting devices. The dosage is the smallest amount capable of providing a diagnostically effective image, and may be determined by means conventional in the art, using known radio-imaging agents as a guide.

Typically, the imaging is carried out on the whole body of the subject, or on that portion of the body or organ relevant to the condition or disease under study. The amount of radio-labeled ABM accumulated at a given point in time in relevant target organs can then be quantified.

A particularly suitable radio-detecting device is a scintillation camera, such as a gamma camera. A scintillation camera is a stationary device that can be used to image distribution of radio-labeled ABM. The detection device in the camera senses the radioactive decay, the distribution of which can be recorded. Data produced by the imaging system can be digitized. The digitized information can be analyzed over time discontinuously or continuously. The digitized data can be processed to produce images,

called frames, of the pattern of uptake of the radio-labelled ABM in the target organ at a discrete point in time. In most continuous (dynamic) studies, quantitative data is obtained by observing changes in distributions of radioactive decay in target organs over time. In other words, a time-activity analysis of the data will illustrate uptake through clearance of the radio-labeled binding protein by the target organs with time.

Various factors should be taken into consideration in selecting an appropriate radioisotope. The radioisotope must be selected with a view to obtaining good quality resolution upon imaging, should be safe for diagnostic use in humans and animals, and should preferably have a short physical half-life so as to decrease the amount of radiation received by the body. The radioisotope used should preferably be pharmacologically inert, and, in the quantities administered, should not have any substantial physiological effect.

The ABM may be radio-labeled with different isotopes of iodine, for example ^{123}I , ^{125}I , or ^{131}I (see for example, U.S. Patent 4,609,725). The extent of radio-labeling must, however be monitored, since it will affect the calculations made based on the imaging results (i.e. a diiodinated ABM will result in twice the radiation count of a similar monoiodinated ABM over the same time frame).

In applications to human subjects, it may be desirable to use radioisotopes other than ^{125}I for labeling in order to decrease the total dosimetry exposure of the human body and to optimize the detectability of the labeled molecule (though this radioisotope can be used if circumstances require). Ready availability for clinical use is also a factor. Accordingly, for human applications, preferred radio-labels are for example, $^{99\text{m}}\text{Tc}$, ^{67}Ga , ^{68}Ga , ^{90}Y , ^{111}In , $^{113\text{m}}\text{In}$, ^{123}I , ^{186}Re , ^{188}Re or ^{211}At .

The radio-labelled ABM may be prepared by various methods. These include radio-halogenation by the chloramine - T method or the lactoperoxidase method and subsequent purification by HPLC (high pressure liquid chromatography), for example as described by J. Gutkowska et al in "Endocrinology and Metabolism Clinics of America: (1987) 16 (1):183. Other known methods of radio-labeling can be used, such as IODOBEADS™.

There are a number of different methods of delivering the radio-labeled ABM to the end-user. It may be administered by any means that enables the active agent to reach the agent's site of action in the body of a mammal. Because proteins are subject to being digested when administered orally, parenteral administration, i.e., intravenous, subcutaneous, intramuscular, would ordinarily be used to optimize absorption of an ABM, such as an antibody, which is a protein.

EXAMPLES

Example 1

Differentially expressed mouse genes, and corresponding human genes/proteins, were identified as described in this Example, and compiled into Master Table 1.

Animal Models Upon separation from their mothers (weaning), C57Bl/6J mice (i.e., C57Bl/6 mice developed by Jackson Labs) were placed on a normal diet (PMI Nutrition International Inc., Brentwood, MO, Prolab RMH3000). Two mice were sacrificed at an average of 35, 49, 77, 118, 133, 207, 403, 558 and 725 days of age.

RNA isolation.

Total RNA was isolated from muscle (gastrocnemius) using the RNA STAT-60 Total RNA/mRNA Isolation Reagent according to the manufacturer's instructions (Tel-Test, Friendswood, TX).

Sample Quantification and Quality Assessment

Total RNA was quantified and assessed for quality on a Bioanalyzer RNA 6000 Nano chip (Agilent). Each chip contained an interconnected set of gel-filled channels that allowed for molecular sieving of nucleic acids. Pin-electrodes in the chip were used to create electrokinetic forces capable of driving molecules through these micro-channels to perform electrophoretic separations. Ribosomal peaks were measured by fluorescence signal and displayed in an electropherogram. A successful total RNA sample featured 2 distinct ribosomal peaks (18S and 28S rRNA).

Biotinylated cRNA Hybridization Target.

Total RNA was prepared for use as a hybridization target as described in the manufacturer's instructions for

CodeLink Expression Bioarrays(TM) (Amersham Biosciences). The CodeLink Expression Bioarrays utilize nucleic acid hybridization of a biotin-labeled complementary RNA (cRNA) target with DNA oligonucleotide probes attached to a gel matrix.

The biotin-labeled cRNA target is prepared by a linear amplification method. Poly (A) + RNA (within the total RNA population) is primed for reverse transcription by a DNA oligonucleotide containing a T7 RNA polymerase promoter 5' to a (dT) 24 sequence. After second-strand cDNA synthesis, the cDNA serves as the template in an *in vitro* transcription (IVT) reaction to produce the target cRNA. The IVT is performed in the presence of biotinylated nucleotides to label the target cRNA. This procedure results in a 50-200 fold linear amplification of the input poly (A) + RNA.

Hybridization Probes.

The oligonucleotide probes were provided by the Codelink Uniset Mouse I Bioarray (Amersham, product code 300013). Amine-terminated oligonucleotide probes are attached to a three-dimensional polyacrylamide gel matrix. There are 10,000 oligonucleotide probes, each specific to a well-characterized mouse gene. Each mouse gene is representative of a unique gene cluster from the fourth quarter 2001 Genbank Unigene build. There are also 500 control probes.

The sequences of the probes are proprietary to Amersham. However, for each probe, Amersham identifies the corresponding mouse gene by NCBI accession number, OGS, LocusLink, Unigene Cluster ID, and description (name). This information should be available from Amersham. In the case of the differentially expressed probes, this information is duplicated in master table 1. For the complete list, see

http://www4.amershambiosciences.com/aptrix/upp01077.nsf/Content/codelink_literature

Under "Gene Lists", select "Uniset Mouse I", and a gene list, in Excel format, can be downloaded.

Hybridization

Using the cRNA target, the hybridization reaction mixture is prepared and loaded into array chambers for bioarray processing as set forth in the manufacturer's instructions for CodeLink Gene Expression Bioarrays™ (Amersham Biosciences). Each sample is hybridized to an individual microarray. Hybridization is at 37°C. The hybridization buffer is prepared as set forth in the Motorola instructions. Hybridization to the microarray is detected with an avidinated fluorescent reagent, Streptavidin-Alexa Fluor® 647 (Amersham).

Mouse Gene Expression Analysis

Processed arrays were scanned using a GenePix 4000B Microarray Scanner (Axon Instruments, Inc.); array images were acquired using the Amersham CodeLink™ Analysis Software (Release 2.2). The Amersham CodeLink™ Analysis Software gives an integrated optical density (IOD) value for every spot; a unique background value for that spot is subtracted, resulting in "raw" data points. Individual chips are then normalized by the Amersham Codelink™ software according to the median raw intensity for all 10,000 genes. A negative control threshold (0.2) is also calculated according to the control probes. A significant difference in expression between samples was defined as a minimum of 2-fold change in expression values. Genes with expression values below the negative control threshold were eliminated from the analysis.

and then the expression data was analyzed to identify genes whose expression levels changed significantly with respect to age.

The list of genes in the tables is a combination of two analyses. Samples of average age 35, 49, 77 and 133 days were compared pair-wise in all possible combinations (6 comparisons) and genes showing differences in expression greater than 2-fold were listed in the table. The remaining samples were divided into three groups (118 days (2 mice): young; 207 and 403 (4 mice) averaged together: medium; 558 and 725 (4 mice) averaged together: old), the three groups were compared in all possible pair-wise combinations (3 comparisons) and genes showing differences in expression greater than 2-fold were added to the table.

Database Searches Nucleotide sequences and predicted amino acid sequences were compared to public domain databases using the Blast 2.0 program (National Center for Biotechnology Information, National Institutes of Health).

Nucleotide database searches were conducted with the then current version of BLASTN 2.0.12, see Altschul, et al., "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.*, 25:3389-3402 (1997). Searches employed the default parameters, unless otherwise stated.

For blastN searches, the default was the blastN matrix (1,-3), with gap penalties of 5 for existence and 2 for extension.

Protein database searches were conducted with the then-current version of BLAST X, see Altschul et al. (1997), supra. Searches employed the default parameters, unless otherwise stated. The scoring matrix was BLOSUM62, with gap costs of 11 for existence and 1 for extension. The standard low complexity filter was used.

"ref" indicates that NCBI's RefSeq is the source database. The identifier that follows is a RefSeq accession number, not a GenBank accession number. "RefSeq sequences are derived from GenBank and provide non-redundant curated data representing our current knowledge of known genes. Some records include additional sequence information that was never submitted to an archival database but is available in the literature. A small number of sequences are provided through collaboration; the underlying primary sequence data is available in GenBank, but may not be available in any one GenBank record. RefSeq sequences are not submitted primary sequences. RefSeq records are owned by NCBI and therefore can be updated as needed to maintain current annotation or to incorporate additional sequence information." See also <http://www.ncbi.nlm.nih.gov/LocusLink/refseq.html>

It will be appreciated by those in the art that the exact results of a database search will change from day to day, as new sequences are added. Also, if you query with a longer version of the original sequence, the results will change. The results given here were obtained at one time and no guarantee is made that the exact same hits would be obtained in a search on the filing date. However, if an alignment between a particular query sequence and a particular database sequence is discussed, that alignment should not change (if the parameters and sequences remain unchanged).

Northern Analysis.

Northern analysis may be used to confirm the results. Favorable and unfavorable genes, identified as described above, or fragments thereof, will be used as probes in Northern hybridization analyses to confirm their differential expression. Total RNA isolated from subject

mice will be resolved by agarose gel electrophoresis through a 1% agarose, 1 % formaldehyde denaturing gel, transferred to positively charged nylon membrane, and hybridized to a probe labeled with [32P] dCTP that was generated from the aforementioned gene or fragment using the Random Primed DNA Labeling Kit (Roche, Palo Alto, CA), or to a probe labeled with digoxigenin according to the manufacturer's instructions (Roche, Palo Alto, CA).

Real-Time RNA Analysis.

Real-time RNA analysis may also be used for confirmation. For "real-time" RNA analysis, RNA will be converted to cDNA and then probed with gene-specific primers made for each clone. "Real-time" incorporation of fluorescent dye will be measured to determine the amount of specific transcript present in each sample. Sample differences (older vs. younger) of 2-fold or greater (in either direction) will be considered differentially expressed. Confirmation using several independent animals is desirable.

In situ Hybridization

Another form of confirmation may be provided by nonisotopic *in situ* hybridizations (NISH) on selected human (obtained by Tissue Informatics) and mouse tissues using cRNA probes generated from mouse genes found to be up- or down-regulated during aging. *In situ* hybridizations may also be performed on mouse tissues using cRNA probes generated from differentially expressed DNAs. These cRNA's will hybridize to their corresponding messenger RNA's present in cells and will provide information regarding the particular cell types within a tissue that is expressing the particular gene as well as the relative level of gene expression. The cRNA probes may be generated by *in vitro*

transcription of template cDNA by Sp6 or T7 RNA polymerase in the presence of digoxigenin-11-UTP (Roche Molecular Biochemicals, Mannheim, Germany; Pardue, M.L. 1985. In: In situ hybridization, Nucleic acid hybridization, a practical approach: IRL Press, Oxford, 179-202).

Transgenic Animals.

Transgenic expression may be used to confirm the results. In one embodiment, a mouse is engineered to overexpress the favorable or unfavorable mouse gene in question. In another embodiment, a mouse is engineered to express the corresponding favorable or unfavorable human gene. In a third embodiment, a nonhuman animal other than a mouse, such as a rat, rabbit, goat, sheep or pig, is engineered to express the favorable or unfavorable mouse or human gene.

Hyperquantitative Tissue Analysis

In addition to gene expression analysis the tissue sections can also be analyzed using TissueInformatics, Inc's TissueAnalytics™ software. A single representative section may be cut from each tissue block, placed on a slide, and stained with H&E. Digital images of each slide may be acquired using an research microscope and digital camera (Olympus E600 microscope and Sony DKC-ST5). These images may be acquired at 20x magnification with a resolution of 0.64 mm/pixel. A hyperquantitative analysis may be performed on the resulting images: First a digital image analysis can identify and annotate structural objects in a tissue using machine vision. These objects, that are constituents of the tissue, can be annotated because they are visually identifiable and have a biological meaning. Subsequently a quantification of these structures regarding their geometric properties like area or stain intensities and their relationship to the field of view or per unit area

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in terms of a % coverage may be performed. Features or parameters for hyper-quantification are specific for each tissue, and may also include relations between features, measures of overall heterogeneity, including orientation, relative locations, and textures.

Correlation Analysis

Mathematical statistics provides a rich set of additional tools to analyze time resolved data sets of hyper-quantitative and gene expression profiles for similarities, including rank correlation, the calculation of regression and correlation coefficients, and clustering. Continuous functions may also be fitted through the data points of individual gene and tissue feature data. Relation between gene expression and hyper-quantitative tissue data may be linear or non-linear, in synchronous or asynchronous arrangements.

The related applications may contain reference to "2-16 week old mice". In the anti-diabetes series of applications, 3 week old mice were put on a diet to induce obesity, hyperinsulinemia and diabetes. The 2-16 week old mice were more accurately described as mice who had been on that diet for 2-16 weeks, i.e., they were actually 5-19 weeks (35-133 days) old. Even some of the anti-aging series of applications made reference to 2-16 week old mice, even though the mice were in fact 5-19 weeks (35-133 days) old.

MASTER TABLE 1: Subtable 1A Favorable Genes/Proteins

Mouse Gene Protein	Unigene	Behavior	Human Proteins	Human Protein Name	Score E (bits) value
NM_009608					
NP_033738.1	Mm.686	F:15.59	NP_005150.1	actin, alpha, cardiac muscle precursor	764 0
			P04270	ACTC_HUMAN Actin, alpha cardiac	764 0
			ATHUC	actin, cardiac muscle	764 0
			AAB59619.1	alpha-cardiac actin	764 0
			AAH09978.1	actin, alpha, cardiac muscle	764 0
			NP_001091.1	alpha 1 actin precursor; alpha skeletal muscle actin	759 0
			P02568	ACTS_HUMAN Actin, alpha skeletal muscle (Alpha-actin 1)	759 0
			ATHU	actin alpha 1, skeletal muscle	759 0
			AAB59376.1	alpha-actin	759 0
			AAA60296.1	alpha-skeletal actin precursor	759 0
			AAF02694.1	AF182035_1 skeletal muscle alpha-actin precursor	759 0
			AAH12597.1	Similar to actin, alpha 1, skeletal muscle	759 0
			NP_001604.1	alpha 2 actin; alpha-cardiac actin	755 0
			P03996	ACTA_HUMAN Actin, aortic smooth muscle (Alpha-actin 2)	755 0
			CAA32064.1	alpha-actin (AA 1-377)	755 0
			AAH17554.1	actin, alpha 2, smooth muscle, aorta	755 0
			ATHUSM	actin alpha 2, aortic smooth muscle	752 0
			AAA51577.1	alpha-actin	752 0
			NP_001606.1	actin, gamma 2 propeptide; actin, alpha-3	750 0
			P12718	ACTH_HUMAN Actin, gamma-enteric smooth muscle (Alpha-actin 3)	750 0
			A40261	actin gamma, enteric smooth muscle	750 0
			CAA34814.1	gamma-actin (AA 1-376)	750 0
			BAA00546.1	enteric smooth muscle gamma-actin	750 0
			AAH12617.1	Similar to actin, gamma 2, smooth muscle, enteric	750 0
			JC5818	gamma-actin	723 0
			NP_001605.1	actin, gamma 1 propeptide; cytoskeletal gamma-actin; actin, cytoplasmic 2	723 0
			P02571	ACTG_HUMAN Actin, cytoplasmic 2	723 0

ATHUG	actin gamma 1	723	0
CAA27723.1	gamma-actin	723	0
AAA51579.1	gamma-actin	723	0
AAH00292.1	actin, gamma 1	723	0
AAH01920.1	actin, gamma 1	723	0
AAH07442.1	actin, gamma 1	723	0
AAH09848.1	actin, gamma 1	723	0
AAH10999.1	Similar to actin, gamma 1	723	0
AAH12050.1	Similar to actin, gamma 1	723	0
AAH15005.1	actin, gamma 1	723	0
AAH15695.1	actin, gamma 1	723	0
AAH15779.1	actin, gamma 1	723	0
AAH18774.1	actin, gamma 1	723	0
NP_001092.1	beta actin; beta cytoskeletal actin	722	0
P02570	ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin)	722	0
ATHUB	actin beta	722	0
CAA25099.1	beta-actin	722	0
AAA51567.1	cytoplasmic beta actin	722	0
AAH01301.1	actin, beta	722	0
AAH02409.1	actin, beta	722	0
AAH04251.1	actin, beta	722	0
AAH13380.1	actin, beta	722	0
AAH14861.1	actin, beta	722	0
AAH16045.1	actin, beta	720	0
CAA45026.1	mutant beta-actin (beta'-actin)	718	0
U08020			
AAA88912.1	Mm.22621 F:11.16 P02452	486 e-136	
	CA11_HUMAN Collagen alpha 1(I) chain precursor		
	alpha 1 type I collagen preproprotein; Collagen I, alpha-1 polypeptide; osteogenesis		
NP_000079.1	imperfecta type IV; collagen of skin, tendon and bone, alpha-1 chain	484 e-136	
CAA98968.1	prepro-alpha1(I) collagen	484 e-136	
CGHU1S	collagen alpha 1(I) chain precursor	483 e-136	
AAA51995.1	alpha 1 (I) chain propeptide	482 e-135	

NM_007743	AAH36531.1	Unknown (protein for MGC:33668)	480 e-135
	AAB27856.1	type I collagen pro alpha 1(I) chain propeptide	469 e-131
	CAA29605.1	C-terminal propeptide domain	435 e-121
	CAA29604.1	pro-alpha 1 (II) collagen (313 AA; AA 975-271c)	372 e-102
	NP_001835.2	alpha 1 type II collagen isoform 1; collagen II, alpha-1 polypeptide; cartilage collagen;	
	AAC41772.1	chondrocalcin, included; COL11A3, formerly	372 e-102
		alpha-1 type II collagen	372 e-102
	AAB69977.1	alpha2(I) collagen	706 0
		alpha 2 type I collagen; Collagen I, alpha-2 polypeptide; Collagen of skin, tendon and	
	NP_000080.1	bone, alpha-2 chain	704 0
NP_031769.1	CAA98969.1	prepro-alpha2(I) collagen	704 0
	CGHU2S	collagen alpha 2(I) chain precursor	699 0
	AAB93981.1	pro-alpha 2(I) collagen	699 0
	P08123	CA21_HUMAN Collagen alpha 2(I) chain precursor	699 0
	CAA23761.1	procollagen (1 is 3rd base in codon)	685 0
	CAA39142.1	type I collagen	553 e-157
		alpha 1 type II collagen isoform 2, preproprotein; collagen II, alpha-1 polypeptide;	
	NP_149162.1	cartilage collagen; chondrocalcin, included; COL11A3, formerly	458 e-128
	P02458	CA12_HUMAN Collagen alpha 1(II) chain precursor [Contains: Chondrocalcin]	458 e-128
	CAA34488.1	prepropeptide (AA 1-1418)	458 e-128
J04694		alpha 1 type IV collagen preproprotein; collagen IV, alpha-1 polypeptide; collagen of	
	NP_001836.1	basement membrane, alpha-1 chain	563 e-160
	P02462	CA14_HUMAN Collagen alpha 1(IV) chain precursor	563 e-160
	CGHU4B	collagen alpha 1(IV) chain precursor	563 e-160
	AAA53098.1	alpha-1 type IV collagen	563 e-160
	CAC13153.1	bA472K17.2 (collagen type IV alpha 1)	563 e-160
	AAH47305.1	Similar to collagen, type IV, alpha 1	563 e-160
	1402236A	collagen alpha1(IV)	563 e-160
	CAA68698.1	alpa1-chain	520 e-147

AAA52006.1	pro-alpha-1(IV)	479 e-134
AAA52042.1	procollagen alpha-1 type IV A Chain A, The 1.9-A Crystal Structure Of The Noncollagenous (Nc1) Domain Of Human Placenta Collagen Iv Shows Stabilization Via A Novel Type Of Covalent Met-Lys Cross-Link	479 e-134
1LI1-	B Chain B, The 1.9-A Crystal Structure Of The Noncollagenous (Nc1) Domain Of Human Placenta Collagen Iv Shows Stabilization Via A Novel Type Of Covalent Met-Lys Cross-Link	474 e-133
1LI1	D Chain D, The 1.9-A Crystal Structure Of The Noncollagenous (Nc1) Domain Of Human Placenta Collagen Iv Shows Stabilization Via A Novel Type Of Covalent Met-Lys Cross-Link	474 e-133
1LI1	E Chain E, The 1.9-A Crystal Structure Of The Noncollagenous (Nc1) Domain Of Human Placenta Collagen Iv Shows Stabilization Via A Novel Type Of Covalent Met-Lys Cross-Link	474 e-133
1LI1	Human Placenta Collagen Iv Shows Stabilization Via A Novel Type Of Covalent Met-Lys Cross-Link	474 e-133
AAF72630.1	Met-Lys Cross-Link	474 e-133
AAK53382.1	AF258349_1 arresten	474 e-133
AAK92480.1	AF363672_1 arresten	474 e-133
AAM97359.1	AF400431_1 arresten	470 e-131
AAA51558.1	alpha-5 type IV collagen	422 e-117
NM_016749	Mm.12561	
NP_058029.1	4	
AAH44226.1	Similar to myosin binding protein H	793
Q13203	MYPH_HUMAN Myosin-binding protein H (MyBP-H) (H-protein)	793
AAB86737.1	myosin binding protein H	784
NP_004988.1	myosin binding protein H; myosin-binding protein H	775
A46118	myosin-binding protein H	775
AAA36339.1	fibronectin type III domains, aa 70-170 and aa 265-365; immunoglobulin C2 domains, aa 185-264 and aa 391-473; 86 kD protein	775
NP_004524.1	myosin binding protein C, fast type; myosin-binding protein C, fast-type; fast-type muscle myosin-binding-protein C	462 e-130

			MYPF_HUMAN Myosin-binding protein C, fast-type (Fast MyBP-C) (C-protein,			
Q14324			skeletal muscle fast-isoform)			462 e-130
S36845			myosin-binding protein C, fast-type muscle			462 e-130
CAA51544.1			fast MyBP-C			462 e-130
			myosin binding protein C, slow type; myosin-binding protein C, slow-type; skeletal			
NP_002456.1			muscle C-protein			459 e-129
S36846			myosin-binding protein C, slow-type muscle			459 e-129
CAA51545.1			slow MyBP-C			459 e-129
CAD38625.1			hypothetical protein			458 e-128
CAD38925.1			hypothetical protein			457 e-128
			MYPS_HUMAN Myosin-binding protein C, slow-type (Slow MyBP-C) (C-protein,			
Q00872			skeletal muscle slow-isoform)			449 e-126
NP_000247.1			protein C, cardiac; myosin-binding protein C, cardiac			445 e-125
			MYPC_HUMAN Myosin-binding protein C, cardiac-type (Cardiac MyBP-C) (C-protein,			
Q14896			cardiac muscle isoform)			445 e-125
S55050			cardiac myosin-binding protein C			445 e-125
CAA58882.1			cardiac myosin-binding protein C			2.00e-
NM_024283						62
NP_077245.1	Mm.11819	F:5.33	NP_115787.1 esophageal cancer related gene 4 protein			236
			AAG42321.1 AF325503_1 esophageal cancer related gene 4 protein			62
			AAH21742.1 esophageal cancer related gene 4 protein			2.00e-
AK017926						236
BAB31006.1	Mm.21697	F:5.21	AAH46217.1 Unknown (protein for MGC:57869)			403 e-112
			NP_061931.1 RTP801			372 e-103
			BAA91214.1 unnamed protein product			372 e-103
			AAH07714.1 hypothetical protein			372 e-103
			AAH15236.1 hypothetical protein			372 e-103
			AAI38424.1 RTP801			372 e-103

NM_009242	AAM10442.1	REDD-1		372 e-103
	CAB66603.1	hypothetical protein		370 e-102
NP_033268.1	NP_003109.1	secreted protein, acidic, cysteine-rich (osteonectin); Osteonectin (secreted protein, acidic, cysteine-rich)		575 e-163
	P09486	SPRC_HUMAN SPARC precursor (Secreted protein acidic and rich in cysteine)		
	GEHUN	(Osteonectin) (ON) (Basement membrane protein BM-40)		575 e-163
	CAA68724.1	osteonectin precursor		575 e-163
	AAA60570.1	extracellular matrix protein BM-40 (AA 1 - 303)		575 e-163
	AAH04974.1	osteonectin		575 e-163
	AAH08011.1	secreted protein, acidic, cysteine-rich (osteonectin)		575 e-163
	AAA60993.1	secreted protein, acidic, cysteine-rich (osteonectin)		575 e-163
	1BMO	osteonectin		573 e-163
	1BMO	A Chain A, Bm-40, FSEC DOMAIN PAIR		496 e-140
	1NUB	B Chain B, Bm-40, FSEC DOMAIN PAIR		496 e-140
	1NUB	A Chain A, Helix C Deletion Mutant Of Bm-40 Fs-Ec Domain Pair		474 e-133
	1NUB	B Chain B, Helix C Deletion Mutant Of Bm-40 Fs-Ec Domain Pair		474 e-133
	AAH33721.1	Unknown (protein for MGC:45264)	5.00e-	87
	NP_004675.2	SPARC-like 1; mast9; hevin	5.00e-	87
	CAA60386.1	Hevin-like protein	5.00e-	87
	Q14515	SPL1_HUMAN SPARC-like protein 1 precursor (High endothelial venule protein) (Hevin) (MAST 9)	5.00e-	87
	S60062	hevin precursor	5.00e-	87
	CAA57650.1	hevin	5.00e-	87

NM_016769	Q92940	Mm.7320	F:4.01	1SRA	Extracellular Matrix Protein Mol_id: 1; Molecule: Sparc; Chain: Null; Fragment: Carboxy-Terminal Domain (Residues 136 - 286); Synonym: Bm-40, Osteonectin; Engineered: Yes; Heterogen: 2 Ca 2+ Ions, One Unidentified Metal Ion Modeled As Ca 2+; Other_details: Crystallized From 0.7 M K, Na-Tartrate, Ph 7.5 + 2 Mm CacI2	311	2.00e-84
NM_016769	Q92940	Mm.7320	F:4.01	AAB18967.1	JV15-2	848	0
				AAB80960.1	hMAD-3	848	0
				BAA22032.1	Smad 3	840	0
				S71798	MAD-3 protein homolog - human	835	0
					MAD, mothers against decapentaplegic homolog 2; MAD (mothers against decapentaplegic, Drosophila) homolog 2; Mothers against		
				NP_005892.1	decapentaplegic, Drosophila, homolog of, 2	757	0
					Mothers against decapentaplegic homolog 2 (SMAD 2) (Mothers against DPP homolog 2) (Mad-related protein 2) (hMAD-2) (JV18-1)		
				Q15796	(hSMAD2)	757	0
				S71797	MAD-2 protein homolog - human	757	0
				AAC50789.1	JV18-1	757	0
NM_016769	Q92940	Mm.7320	F:4.01	AAB17087.1	mad protein homolog	757	0
				AAB17054.1	MAD-related protein 2	757	0
				AAC51918.1	MAD-related protein Smad2	757	0
				AAC39657.1	Smad2	757	0
				AAH14840.1	MAD, mothers against decapentaplegic homolog 2	757	0
				AAH25699.1	MADH2 protein	757	0
				AAP36090.1	MAD, mothers against decapentaplegic homolog 2 (Drosophila)	757	0
				AAB92396.1	SMAD5	515	e-145
					Mothers against decapentaplegic homolog 5 (SMAD 5) (Mothers against DPP homolog 5) (Smad5) (hSmad5) (JV5-1)		
				Q99717	DPP homolog 5) (Smad5) (hSmad5) (JV5-1)	515	e-145
NM_016769	Q92940	Mm.7320	F:4.01	AAB95090.1	Smad5; MAD-like protein	515	e-145
				AAB72180.1	Smad5	515	e-145

AAB66353.1	Smad5		515	e-145
AAH09682.1	MAD, mothers against decapentaplegic homolog 5		515	e-145
AAB82655.1	Mad homolog		515	e-145
AAC50791.1	Smad5		513	e-144
	MAD, mothers against decapentaplegic homolog 1; MAD (mothers against decapentaplegic, Drosophila) homolog 1; Mothers against decapentaplegic, Drosophila, homolog of, 1		507	e-143
NP_005891.1	Q15797Mothers against decapentaplegic homolog 1 (SMAD 1) (Mothers against DPP homolog 1) (Mad-related protein 1) (Transforming growth factor-beta signaling protein-1) (BSP-1) (hSMAD1)		507	e-143
Q15797	transcription activator Smad1 - human		507	e-143
S68987	mad-related protein MADR1		507	e-143
AAC50493.1	Smad1		507	e-143
AAB06852.1	transforming growth factor-beta signaling protein-1		507	e-143
AAC50621.1	Smad1		507	e-143
AAC50790.1	MAD, mothers against decapentaplegic homolog 1		507	e-143
AAH01878.1	MAD, mothers against decapentaplegic homolog 1		507	e-143
	against			
	decapentaplegic homolog 1		507	e-143
	MAD, mothers against decapentaplegic homolog 9; MAD (mothers against decapentaplegic, Drosophila) homolog 9; Mothers against decapentaplegic, drosophila, homolog of, 9		505	e-142
NP_005896.1	mother against dpp (Mad) related protein		505	e-142
BAA21129.1	MAD, mothers against decapentaplegic homolog 9		505	e-142
AAH11559.1			2.00e-	
NM_009876	Mm.16878		228	59
NP_034006.1	F:3.92 NP_000067.1 cyclin-dependent kinase inhibitor 1C; Beckwith-Wiedemann syndrome			

Accession	Gene Symbol	Protein Name	Function	Length (aa)	Molecular Weight (kDa)	Isoelectric Point (pI)	Instability
P49918	CDNC_HUMAN	Cyclin-dependent kinase inhibitor 1C (Cyclin-dependent kinase inhibitor p57) (p57KIP2)		228	22.00	5.9	2.00e-59
G02424		cyclin-dependent kinase inhibitor 1C		228	22.00	5.9	2.00e-59
AAA85095.1		p57KIP2		228	22.00	5.9	2.00e-59
AAB05896.1		cdk-inhibitor p57/KIP2		228	22.00	5.9	2.00e-59
BAA11014.1		p57KIP2		228	22.00	5.9	2.00e-59
BAA11015.1		p57KIP2		226	6.00	5.9	6.00e-59
AF064749							
AAC23667.1	Mm.7562	F:3.77	NP_476506.1 alpha 3 type VI collagen isoform 3 precursor; collagen VI, alpha-3 polypeptide	2289	0		0
			NP_004360.1 alpha 3 type VI collagen isoform 1 precursor; collagen VI, alpha-3 polypeptide	2119	0		0
			P12111 CA36_HUMAN Collagen alpha 3(VI) chain precursor	2119	0		0
			CGHU3A collagen alpha 3(VI) chain precursor [validated]	2119	0		0
			CAA36267.1 collagen type VI, alpha 3 chain	2119	0		0
			NP_476507.1 alpha 3 type VI collagen isoform 4 precursor; collagen VI, alpha-3 polypeptide	2119	0		0
			NP_476508.1 alpha 3 type VI collagen isoform 5 precursor; collagen VI, alpha-3 polypeptide	2119	0		0
			NP_476505.1 alpha 3 type VI collagen isoform 2 precursor; collagen VI, alpha-3 polypeptide	1565	0		0
			AAH33174.1 Similar to collagen, type VI, alpha 3	978	0		0
NM_010436	Mm.24593						
P27661	1	F:3.76	NP_002096.1 H2A histone family, member X; H2AX histone	230	4e-060		230 4e-060
			P16104 Histone H2A.x (H2a/x)	230	4e-060		230 4e-060
			S07631 histone H2A.X - human	230	4e-060		230 4e-060
			CAA32968.1 unnamed protein product	230	4e-060		230 4e-060
			AAH04915.1 H2A histone family, member X	230	4e-060		230 4e-060
			AAH11694.1 H2A histone family, member X	230	4e-060		230 4e-060

NM_007632	Mm.16999	AAH13416.1	H2A histone family, member X	230 4e-060
P30282	8	F:3.45		
		NP_001751.1	cyclin D3; D3-type cyclin; G1/S-specific cyclin D3	484 e-136
		P30281	G1/S-specific cyclin D3	484 e-136
		AAA52137.1	cyclin D3	484 e-136
		AAH11616.1	cyclin D3	484 e-136
		B42822	cyclin D3 - human	484 e-136
		AAA51927.1	D3-type cyclin	484 e-136
		AAM51826.1	cyclin D3	484 e-136
		AAA51929.1	cyclin D3	332 1e-090
		NP_001750.1	cyclin D2; G1/S-specific cyclin D2	308 2e-083
		P30279	G1/S-specific cyclin D2	308 2e-083
		A42822	cyclin D2 - human	308 2e-083
		CAA48493.1	cyclin D2	308 2e-083
		AAA51926.1	D-type cyclin	308 2e-083
		BAA02802.1	KIAK0002	308 2e-083
		AAH10958.1	Cyclin D2	308 2e-083
		AAM54041.1	Cyclin D2	308 2e-083
		AAA51928.1	cyclin D2	285 1e-076
		NP_444284.1	cyclin D1; G1/S-specific cyclin D1; B-cell CLL/lymphoma 1	253 8e-067
		P24385	G1/S-specific cyclin D1 (PRAD1 oncogene) (BCL-1 oncogene)	253 8e-067
		A38977	cyclin D1 - human	253 8e-067
		CAA42470.1	cyclin	253 8e-067
		AAA58392.1	bcl-1	253 8e-067
		CAA80558.1	cyclin	253 8e-067
		AAH00076.1	Cyclin D1	253 8e-067
		AAH14078.1	Cyclin D1	253 8e-067
		AAH01501.1	Cyclin D1	253 8e-067
		AAH25302.1	Cyclin D1	253 8e-067
		AAM34300.2	Cyclin D1	253 8e-067

NM_010560 I49699	AAH23620.1	Cyclin D1	253 8e-067
	1709356A	cyclin PRAD1	253 8e-067
	AAA52136.1	cyclin D	250 7e-066
		interleukin 6 signal transducer isoform 1 precursor; membrane	
		glycoprotein gp130; oncostatin M receptor; CD130 antigen;	
		interleukin receptor beta chain; gp130 transducer chain;	
		gp130 of the rheumatoid arthritis antigenic	
		peptide-bearing soluble form	
	NP_002175.2	Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin	1328 0
		6 signal transducer) (Membrane glycoprotein 130) (gp130)	
	P40189	(Oncostatin M receptor) (CDw130) (CD130 antigen)	1327 0
	A36337	membrane glycoprotein gp130 precursor - human	1327 0
	AAA59155.1	membrane glycoprotein 130	1327 0
		interleukin 6 signal transducer isoform 2 precursor; membrane	
		glycoprotein gp130; oncostatin M receptor; CD130 antigen;	
		interleukin receptor beta chain; gp130 transducer chain;	
		gp130 of the rheumatoid arthritis antigenic	
		peptide-bearing soluble form	
	NP_786943.1	gp130 of the rheumatoid arthritis antigenic peptide-bearing soluble	467 e-131
		form (gp130-RAPS)	
	BAA78112.1	Chain A, Crystal Structure Of A CytokineRECEPTOR COMPLEX	466 e-130
	111R	Chain A, Crystal Structure Of The Hexameric Human IL-6IL-6 Alpha	445 e-124
	1P9M	ReceptorGP130 COMPLEX	436 e-121
	pdb 1BQU A	Chain A, Cytokine-Binding Region Of Gp130	310 1e-083
	pdb 1BQU B	Chain B, Cytokine-Binding Region Of Gp130	310 1e-083
		Chain A, Crystal Structure Of Leukemia Inhibitory Factor In Complex	
		With Gp130	
	pdb 1PVI A		289 3e-077

Chain C, Crystal Structure Of Leukemia Inhibitory Factor In Complex			
pd11PVHJC	With Gp130		289 3e-077
gp130-like monocyte receptor; soluble type I cytokine receptor CRL3;			
NP_620586.2	GP130 like receptor		223 3e-057
AAM27958.1	gp130-like monocyte receptor		223 3e-057
AAQ88484.1	GLM-R		223 3e-057
colony stimulating factor 3 receptor isoform a precursor; granulocyte			
NP_000751.1	colony stimulating factor receptor; CD114 antigen		210 2e-053
GCSR_HUMAN Granulocyte colony stimulating factor receptor precursor (G-CSF-R)			
Q99062	(CD114 antigen)		210 2e-053
CAA39253.1	granulocyte colony stimulating factor receptor 25-1		210 2e-053
AAA63176.1	granulocyte colony-stimulating factor receptor		210 2e-053
AAN05790.1	colony stimulating factor 3 receptor (granulocyte)		210 2e-053
AAH53585.1	Colony stimulating factor 3 receptor, isoform a precursor		210 2e-053
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation			
NM_018871	protein, gamma polypeptide; 14-3-3 gamma	Mm.28498	462 e-129
P35214	14-3-3 protein gamma (Protein kinase C inhibitor protein-1)	F:3.35	462 e-129
P35214	(KCIP-1)		462 e-129
BAA85184.1	14-3-3gamma		462 e-129
Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation			
AAH20963.1	protein, gamma polypeptide		462 e-129
AAD48408.1	14-3-3 gamma protein		422 e-117
tyrosine 3/tryptophan 5 -monooxygenase activation protein, eta			
NP_003396.1	polypeptide; 14-3-3 eta		407 e-113
Q04917	14-3-3 protein eta (Protein AS1)		407 e-113
S38509	14-3-3 protein eta chain - human		407 e-113
CAA55017.1	14-3-3 eta subtype		407 e-113
CAA56676.1	14-3-3 protein		407 e-113
AAB36036.1	14.3.3 eta chain		407 e-113

BAA11418.1	14-3-3 protein eta chain	407	e-113
	cN44A4.1 (tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein, eta polypeptide (14-3-3 protein ETA))		
CAB05112.1	Tyrosine 3/tryptophan 5 -monoxygenase activation protein, eta polypeptide	407	e-113
AAH03047.1	14-3-3n	407	e-113
AAA35483.1	protein 14-3-3 eta chain - human	406	e-112
S38532	tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein, beta polypeptide; 14-3-3 protein beta/alpha; protein kinase C inhibitor protein-1; protein 1054; brain protein 14-3-3, beta isoform	401	e-111
NP_003395.1	dJ148E22.1 (Tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein, beta polypeptide, isoform 1)	348	4e-095
CAA15497.1	activation protein, beta polypeptide, isoform 1)	348	4e-095
CAA40620.1	AS1	347	8e-095
AAH63824.1	Unknown (protein for IMAGE:6180974)	346	1e-094
AAH51814.1	YWHAZ protein	346	1e-094
AAH03623.2	YWHAZ protein	346	1e-094
	signal transducer and activator of transcription 5B; transcription factor STAT5B		
NP_036580.2	factor STAT5B	1510	0
P51692	Signal transducer and activator of transcription 5B	1510	0
AAC50485.2	transcription factor Stat5b	1510	0
CAD19638.1	STAT5B_CDS	1510	0
AAH65227.1	Unknown (protein for MGC:74606)	1510	0
AAC50491.1	signal transducer and activator of transcription Stat5B	1510	0
NP_003143.2	signal transducer and activator of transcription 5A	1508	0
P42229	Signal transducer and activator of transcription 5A	1405	0
AAA73962.1	signal transducer and activator of transcription	1405	0
AAH27036.1	Signal transducer and activator of transcription 5A	1405	0

NIM_011489

I49274

Mm.34064 F:3.26

NP_002602.2	pyruvate dehydrogenase kinase, isoenzyme 2	556	e-157
	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 2, mitochondrial		
Q15119	precursor (Pyruvate dehydrogenase kinase isoform 2)	556	e-157
AAH05811.1	Pyruvate dehydrogenase kinase, isoenzyme 2	556	e-157
AAH40478.1	PK2 protein	556	e-157
I70159	[pyruvate dehydrogenase (lipoamide)] kinase (EC 2.7.1.99) 2 - human	554	e-157
AAC42010.1	pyruvate dehydrogenase kinase	554	e-157
2203383B	pyruvate dehydrogenase kinase:ISOTYPE=2	554	e-157
AAH63137.1	Pyruvate dehydrogenase kinase, isoenzyme 2	553	e-157
NP_005382.1	pyruvate dehydrogenase kinase, isoenzyme 3	527	e-149
	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 3, mitochondrial		
Q15120	precursor (Pyruvate dehydrogenase kinase isoform 3)	527	e-149
I70160	[pyruvate dehydrogenase (lipoamide)] kinase (EC 2.7.1.99) 3 - human	527	e-149
AAC42011.1	pyruvate dehydrogenase kinase	527	e-149
AAH15948.1	Pyruvate dehydrogenase kinase, isoenzyme 3	527	e-149
2203383C	pyruvate dehydrogenase kinase:ISOTYPE=3	527	e-149
AK013885	Mm.15337		
NP_082503.1	2	914	0
	F:3.16 NP_006759.2 BRCA1 associated protein		
	AAP93638.1 impedes mitogenic signal propagation	914	0
	AAC24200.1 BRCA1-associated protein 2	857	0
	AAB88538.1 putative DDB p127-associated protein	410	e-114
NM_019704	Mm.26015		
NP_062678.1	3	491	e-138
	F:3.12 NP_008955.1 PL6 protein		
	Q12893 PL6_HUMAN PL6 protein (Placental protein 6)	491	e-138
	G01430 PL6 protein - human	491	e-138
	AA92281.1 PL6 protein	491	e-138
	AAH11948.1 PL6 protein	491	e-138
	AAH17367.1 PL6 protein	491	e-138
	AAB67308.1 PL6 protein, unknown function but deleted in small cell lung cancer	332	1e-090

AK005449	Mm.18755						198 7e-051
BAB24042.1	4	F:3.1	AAQ15212.1	FP291	platelet-derived growth factor receptor-like protein; platelet-derived growth		
AK004179							
BAB23210.1	Mm.28951	F:3.05	NP_006198.1		factor-beta-like tumor suppressor	645	0
			I60125		PDGF receptor beta-like tumor suppressor	645	0
			BAA07179.1		PDGF receptor beta-like tumor suppressor	645	0
			AAH10927.1		Similar to platelet-derived growth factor receptor-like	645	0
NM_008684							
P97798	Mm.42249	F:3.04	AAC51287.1		neogenin	2554	0
			NP_002490.1		neogenin homolog 1; neogenin (chicken) homolog 1	2554	0
			Q92859		Neogenin precursor	2554	0
			AAB17263.1		neogenin	2554	0
			NP_005206.1		deleted in colorectal carcinoma	1303	0
			P43146		Tumor suppressor protein DCC precursor (Colorectal cancer suppressor)	1303	0
			A54100		tumor suppressor protein DCC precursor - human	1303	0
			CAA53735.1		tumour suppressor	1303	0
			AAA35751.1		colorectal tumor suppressor (put.); putative	760	0
					protein tyrosine phosphatase, receptor type, D isoform 2 precursor;		
					protein tyrosine phosphatase, receptor type, delta		
			NP_569075.1		polypeptide; protein tyrosine phosphatase delta	271 1e-071	
					protein tyrosine phosphatase, receptor type, D isoform 1 precursor;		
					protein tyrosine phosphatase, receptor type, delta		
			NP_002830.1		polypeptide; protein tyrosine phosphatase delta	265 8e-070	
			P23468		Protein-tyrosine phosphatase delta precursor (R-PTP-delta)	265 8e-070	
					protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta		
			A56178		precursor - human	265 8e-070	
			AAC41749.1		protein tyrosine phosphatase delta	265 8e-070	
			NP_066013.1		DDM36	261 1e-068	
			BAB86306.1		hDDM36	261 1e-068	

NP_570924.1	protein tyrosine phosphatase, receptor type, sigma isoform 2 precursor; protein tyrosine phosphatase PTPsigma	253	3e-066
NP_569076.1	protein tyrosine phosphatase, receptor type, D isoform 3 precursor; protein tyrosine phosphatase, receptor type, delta polypeptide; protein tyrosine phosphatase delta	250	2e-065
Q13332	Receptor-type protein-tyrosine phosphatase S precursor (R-PTP-S)	245	5e-064
AAC50299.1	(Protein-tyrosine phosphatase sigma)	245	5e-064
2204414A	protein tyrosine phosphatase sigma	245	5e-064
NP_009825	protein Tyr phosphatase		
NP_033955.1	Unknown (protein for IMAGE:4748644)	731	0
AAH36298.1	serine (or cysteine) proteinase inhibitor, clade H, member 1; collagen-binding protein		
NP_004344.1	1; gp46; colligin-1; collagen-binding protein 2; colligin-2; heat shock protein 47	726	0
P29043	HS47_HUMAN 47 kDa heat shock protein precursor (Collagen-binding protein 1)		
S20608	(Colligin 1)	726	0
CAA43795.1	heat shock protein Hsp47 precursor	726	0
P50454	colligin	726	0
BAA96788.1	CBP2_HUMAN Collagen-binding protein 2 precursor (Colligin 2) (Rheumatoid arthritis related antigen RA-A47)	723	0
BAA96789.1	rheumatoid arthritis related antigen RA-A47	723	0
AAH14623.1	rheumatoid arthritis related antigen RA-A47	723	0
NP_001226.1	Unknown (protein for MGC:4258)		
I52968	serine (or cysteine) proteinase inhibitor, clade H, member 1; collagen-binding protein		
BAA11829.1	1; gp46; colligin-1; collagen-binding protein 2; colligin-2; heat shock protein 47	719	0
	colligin-2	719	0
	collagen binding protein 2	719	0
BAA96790.1	collagen binding protein 2		5.00e-
	rheumatoid arthritis-related antigen RA-A47	347	95

Accession	Gene	Protein	Function	Score
AA690621	Mm.29470	BAA96791.1	rheumatoid arthritis related antigen RA-A47	5.00e-347 95
XP_207091	9	F:3		
		AAD27717.1	CGI-08 protein	216 1e-056
		CAB59979.1	putative metal transporter	216 1e-056
		CAB59980.1	putative metal transporter	216 1e-056
		AAD34066.1	CGI-71 protein	216 1e-056
		AAH03152.1	SLC39A1 protein	216 1e-056
			solute carrier family 39 (zinc transporter), member 1; zinc-iron regulated transporter-like gene; solute carrier family 39 (zinc transporter), member 3; zinc/iron regulated transporter-like	
		NP_055252.2	Zinc transporter ZIP1 (Zinc-iron regulated transporter-like)	216 1e-056
		Q9NY26	(CGI-08/CGI-71) (hZIP1)	216 1e-056
		CAB82784.1	IRT1 protein	216 1e-056
		AAH02563.1	Solute carrier family 39 (zinc transporter), member 1	216 1e-056
		AAH07886.1	Solute carrier family 39 (zinc transporter), member 1	216 1e-056
		AAH14303.1	Solute carrier family 39 (zinc transporter), member 1	216 1e-056
		BAC11502.1	unnamed protein product	213 8e-056
NM_009464				
P56501	Mm.6254	F:2.99		
		NP_003347.1	uncoupling protein 3 isoform UCP3L; Uncoupling protein-3	531 e-150
		P55916	Mitochondrial uncoupling protein 3 (UCP 3)	531 e-150
		JC5522	uncoupling protein UCP3, mitochondrial - human	531 e-150
		AAC51367.1	UCP3	531 e-150
		AAC51369.1	uncoupling protein 3	531 e-150
		AAC51767.1	uncoupling protein 3	531 e-150
		AAG02284.1	uncoupling protein 3	531 e-150
		AAC18822.1	uncoupling protein 3	525 e-148
		AAC51785.1	uncoupling protein 3	510 e-144

				NP_073714.1	uncoupling protein 3 isoform UCP3S; Uncoupling protein-3	464	e-130
				AAB48411.1	uncoupling protein-2	457	e-128
				NP_003346.2	uncoupling protein 2; Uncoupling protein-2	456	e-128
				P55851	Mitochondrial uncoupling protein 2 (UCP 2) (UCPH)	456	e-128
				AAC51336.1	UCP2	456	e-128
				AAC39690.1	uncoupling protein 2	456	e-128
				AAD21151.1	uncoupling protein 2	456	e-128
				AAH11737.1	uncoupling protein 2	456	e-128
				AAB53091.1	uncoupling protein homolog	456	e-128
				CAA11402.1	uncoupling protein 2	456	e-128
				NP_068605.1	uncoupling protein 1; mitochondrial brown fat uncoupling protein	345	3e-094
				G01858	uncoupling protein 1, mitochondrial - human	345	3e-094
				AAA85271.1	uncoupling protein	345	3e-094
				P25874	Mitochondrial brown fat uncoupling protein 1 (UCP 1) (Thermogenin)	342	2e-093
				CAA36214.1	uncoupling protein	342	2e-093
				AAH08392.1	UCP3 protein	214	7e-055
Z34532							
Q62165	Mm.7524	F:2.98		AAH12740.1	Dystroglycan 1 precursor	431	e-120
				AAH14616.1	Dystroglycan 1 precursor	431	e-120
					dystroglycan 1 precursor; 156DAG; Dystrophin-associated glycoprotein-1; alpha-dystroglycan	431	e-120
				NP_004384.1	Dystroglycan precursor (Dystrophin-associated glycoprotein 1)		
				Q14118	[Contains: Alpha-dystroglycan (Alpha-DG);	431	e-120
				I54343	dystroglycan - human	431	e-120
				AAA81779.1	dystroglycan	431	e-120
NM_011986	Mm.29939						
NP_036116	1	F:2.95		NP_055099.1	neurochondrin	1317	0
				BAA77830.1	neurochondrin-1	1317	0
				BAA85384.2	neurochondrin-1	1317	0

	AAH24592.1	neurochondrin			1317	0
	AAD05029.1	unknown			1312	0
	BAA25533.1	KIAA0607 protein			1296	0
	BAA77831.1	neurochondrin-2			1285	0
	BAA85385.2	neurochondrin-2			1285	0
NM_011817					2.00e-	85
NP_035947.1	Mm.9653	F:2.93	BAA84543.1	gadd45-related protein	313	85
				growth arrest and DNA-damage-inducible, gamma; GADD45-gamma; gadd-related	1.00e-	83
			NP_006696.1	protein, 17 kD	307	83
			O95257	G45G_HUMAN Growth arrest and DNA-damage-inducible protein GADD45 gamma	1.00e-	83
				(Cytokine responsive protein CR6)	307	83
					1.00e-	83
			AAC83329.1	growth arrest and DNA-damage-inducible protein GADD45gamma	307	83
					1.00e-	83
			AAD28544.1	AF079806_1 cytokine responsive protein	307	83
					1.00e-	83
			AAF73468.1	AF265659_1 GADD45 gamma	307	83
					1.00e-	83
			AAH00465.1	growth arrest and DNA-damage-inducible, gamma	307	83
					1.00e-	83
			AAH19325.1	growth arrest and DNA-damage-inducible, gamma	307	83
					1.00e-	83
			AAM00007.1	growth arrest and DNA-damage-inducible, gamma	307	83
					3.00e-	82
			AAK00414.1	AF087883_1 growth arrest and DNA damage inducible protein gamma	303	82
NM_011923	Mm.20891				897	0
Q9R045	9	F:2.93	NP_036230.1	angiopoietin-like 2 precursor; angiopoietin-related protein 2		

Angiopoietin-related protein 2 precursor (Angiopoietin-like 2)				
Q9UKU9	(UNQ170/PRO196)			897 0
AAD55357.1	angiopoietin-related protein-2			897 0
AAH12368.1	Angiopoietin-like 2 precursor			897 0
AAQ88641.1	NL1			897 0
NP_004664.1	angiopoietin-like 1 precursor; angiopoietin 3; angiopoietin Y1			547 e-155
AAD19608.1	angiopoietin Y1			547 e-155
CAC13169.1	dJ595C2.2 (angiopoietin Y1)			547 e-155
BAB40691.1	angiopoietin-related protein 1			547 e-155
AAH50640.1	ANGPTL1 protein			547 e-155
AAQ88645.1	NL5			547 e-155
BAC11358.1	unnamed protein product			521 e-147
BAC11164.1	unnamed protein product			432 e-120
NP_114123.2	angiopoietin-like 6; angiopoietin-related protein 5			400 e-111
BAB91248.1	AGF			400 e-111
AAQ88643.1	NL8			400 e-111
AAK06404.1	angiopoietin-related protein 5			398 e-110
AAQ88678.1	NL7			212 2e-054
NP_116232.2	fibrinogen C domain containing 1			212 2e-054
AAH32953.1	fibrinogen C domain containing 1			212 2e-054
AAH07047.1	Fibrinogen-like 1 precursor			204 5e-052
AAP35281.1	fibrinogen-like 1			204 5e-052
JN0596	fibrinogen-related protein HFREP-1 precursor - human			204 5e-052
BAA03336.1	unknown protein precursor			204 5e-052
NM_008854				
P05132	Mm.19111 F:2.92			692 0
P17612	NP_002721.1 protein kinase, cAMP-dependent, catalytic, alpha			692 0
	cAMP-dependent protein kinase, alpha-catalytic subunit (PKA C-alpha)			
	protein kinase (EC 2.7.1.37), cAMP-dependent, alpha catalytic chain - human			
OKHU2C	human			692 0
CAA30597.1	unnamed protein product			692 0

AAH39846.1	Protein kinase, cAMP-dependent, catalytic, alpha	692	0
NP_002722.1	protein kinase, cAMP-dependent, catalytic, beta isoform b	649	0
P22694	cAMP-dependent protein kinase, beta-catalytic subunit (PKA C-beta)	649	0
	protein kinase (EC 2.7.1.37), cAMP-dependent, beta catalytic chain -		
OKHUCB	human	649	0
AAA60170.1	cAMP-dependent protein kinase catalytic subunit	649	0
AAH35058.1	PRKACB protein	643	0
NP_891993.1	protein kinase, cAMP-dependent, catalytic, beta isoform a	637	0
CAD97818.1	hypothetical protein	637	0
CAE46017.1	hypothetical protein	637	0
	protein kinase (EC 2.7.1.37), cAMP-dependent, gamma catalytic chain -		
OKHUCG	human	599	e-171
AAC41690.1	protein kinase A gamma-subunit	599	e-171
	protein kinase, cAMP-dependent, catalytic, gamma; PKA C-gamma;		
NP_002723.2	serine(threonine) protein kinase	596	e-170
P22612	cAMP-dependent protein kinase, gamma-catalytic subunit (PKA C-gamma)	596	e-170
CAA04863.1	cAMP-dependent protein kinase gamma isoform	596	e-170
AAH39888.1	Protein kinase, cAMP-dependent, catalytic, gamma	595	e-170
AAH16285.1	PRKACB protein	467	e-131
	protein kinase (EC 2.7.1.37), cAMP-dependent, alpha catalytic		
A38143	chain, short splice form - human (fragment)	389	e-107
AAA60094.1	protein kinase A-alpha	389	e-107
NP_005035.1	protein kinase, X-linked	370	e-102
P51817	Serine/threonine protein kinase PRKX (Protein kinase PKX1)	370	e-102
I38121	protein kinase - human	370	e-102
CAA59733.1	protein kinase	370	e-102
AAH41073.1	Protein kinase, X-linked	370	e-102
NM_007737		1247	0
NP_031763.1	type V preprocollagen alpha 2 chain		

		alpha 2 type V collagen preproprotein; Collagen V, alpha-2 polypeptide; AB collagen;		
		NP_000384.1 collagen, fetal membrane, A polypeptide	1224	0
		P05997 CA25_HUMAN Collagen alpha 2(V) chain precursor	1224	0
		CGHU2V collagen alpha 2(V) chain precursor	1224	0
		CAA75002.1 procollagen alpha 2(V)	1224	0
		CAA28454.1 pro- alpha (V)collagen (AA 1099)	1063	0
		AAA52058.1 alpha-2 type V collagen	518 e-146	
		alpha 1 type II collagen isoform 1; collagen II, alpha-1 polypeptide; cartilage collagen;		
		NP_001835.2 chondrocalcin, included; COL11A3, formerly	468 e-131	
		AAC41772.1 alpha-1 type II collagen	468 e-131	
		alpha 1 type II collagen isoform 2, preproprotein; collagen II, alpha-1 polypeptide;		
		NP_149162.1 cartilage collagen; chondrocalcin, included; COL11A3, formerly	468 e-131	
		CAA34683.1 COL2A1	468 e-131	
		CGHU6C collagen alpha 1(II) chain precursor	462 e-129	
		P02458 CA12_HUMAN Collagen alpha 1(II) chain precursor [Contains: Chondrocalcin]	462 e-129	
		CAA34488.1 prepropeptide (AA 1-1418)	462 e-129	
		glycerol-3-phosphate dehydrogenase 1 (soluble); Glycerol-3-phosphate		
NM_010271	Mm.25239			
P13707	1	F.2.9 dehydrogenase, soluble	667	0
		Glycerol-3-phosphate dehydrogenase 1 (soluble)	667	0
		Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic (GPD-C)		
		P21695 (GPDH-C)	667	0
		S55920 glycerol-3-phosphate dehydrogenase (NAD) (EC 1.1.1.8) - human	667	0
		AAA92863.1 L-glycerol-3-phosphate:NAD oxidoreductase	667	0
		2113206A alpha glycerol phosphate dehydrogenase	667	0
		NP_055956.1 KIAA0089 protein	523 e-148	
		AAH28726.1 KIAA0089 protein	523 e-148	
		BAA07648.1 KIAA0089	523 e-148	
		AAH06168.1 Unknown (protein for IMAGE:3960207)	404 e-112	

NM	NP	F	Mm				
NM_008409							
NP_032435.1	NP_004858.1	F:2.89	Mm.193	O43736	integral membrane protein 2A	483 e-136	
	AAC39867.1			E25 protein	ITMA_HUMAN Integral membrane protein 2A (E25 protein)	483 e-136	
	AAH40437.1			integral membrane protein 2A		483 e-136	
NM_027910							
NP_082186.1	NP_476502.1	F:2.88	Mm.45101	testis intracellular mediator protein		768	0
	AAH00295.1			testis intracellular mediator protein		768	0
	AAH01789.1			testis intracellular mediator protein		768	0
	AAH01793.1			testis intracellular mediator protein		768	0
	AAH07296.1			testis intracellular mediator protein		768	0
	BAB63257.1			PEAS		768	0
	AAH21546.1			Testis intracellular mediator protein		768	0
	AAH09460.1			KLHDC3 protein		762	0
	BAC05149.1			unnamed protein product		548	e-155
	AAH41793.1			KLHDC3 protein		463	e-130
	AAH45612.1			KLHDC3 protein		463	e-130
	AAH12987.1			KLHDC3 protein		355	e-113
NM_022318			Mm.28685				
NP_071713.1	NP_071418.2	F:2.87	8	popeye protein 2		533	e-151
	Q9HBU9			Popeye domain containing protein 2 (Popeye protein 2)		533	e-151
	AAH44929.1			Popeye protein 2		533	e-151
	AAG23406.1			Popeye protein 2		521	e-147
	NP_071756.2			Popeye protein 3		280	6e-075
	Q9HBV1			Popeye domain containing protein 3		280	6e-075
	AAH22323.1			Popeye protein 3		280	6e-075
	AAG23404.1			popeye protein 3		277	5e-074
	AAH26911.1			POPDC2 protein		203	8e-052
NM_010514						4.00e-	
NP_034644.1	NP_000603.1	F:2.86	Mm.3862	insulin-like growth factor 2 (somatomedin A); somatomedin A		255	67

P01344	IGF2_HUMAN Insulin-like growth factor II precursor (IGF-II) (Somatomedin A)	255	4.00e-67
IGHU2	insulin-like growth factor II precursor	255	4.00e-67
CAA25426.1	IGF-II precursor	255	4.00e-67
CAA29516.1	precursor polypeptide (AA -24 to 156)	255	4.00e-67
AAA52442.1	preproinsulin-like growth factor II, domains A-E	255	4.00e-67
AAA52535.1	insulin-like growth factor	255	4.00e-67
AAA52545.1	insulin-like growth factor II precursor	255	4.00e-67
AAA60088.1	insulin-like growth factor II	255	4.00e-67
AAB34155.1	insulin-like growth factor II; IGF-II	255	4.00e-67
AAG17220.1	AF217977_1 unknown	255	4.00e-67
AAH00531.1	insulin-like growth factor 2 (somatomedin A)	255	4.00e-67
AAM51825.1	AF517226_1 insulin-like growth factor 2 (somatomedin A)	255	4.00e-67
1009249A	insulin-like growth factor II precursor	255	4.00e-67
1203258B	insulin-like growth factor II	255	4.00e-67

NM_013818	O08582	Mm.19080 F:2.86	AAA52544.1	Insulin-like growth factor II precursor	254	1.00e-	66
			I67610	insulin-like growth factor II, domains A-E	250	1.00e-	65
			AAA52443.1	preproinsulin-like growth factor II, domains A-E	250	1.00e-	65
			S02423	insulin-like growth factor II precursor, splice form II	249	2.00e-	65
			CAA27249.1	put. IGF-II	249	3.00e-	65
			CAA29517.1	precursor polypeptide (AA -24 to 140)	223	2.00e-	57
			NP_004277.1	GTP binding protein 1; G-protein 1	984	0	0
			O00178	GTP-binding protein 1 (G-protein 1) (GP-1) (GP1)	984	0	0
			AAB51273.1	putative G-protein	984	0	0
			CAB42864.1	dJ50815.3 (GTP binding protein 1)	984	0	0
			AAH14075.1	GTP binding protein 1	984	0	0
			JC5291	GTP-binding protein GP-1 - human	984	0	0
			PC7084	GTP-binding protein 2 - human (fragment)	441	e-123	0
			AAF78884.1	putative GTP-binding protein	441	e-123	0
			CAC36269.1	bA22/24.2.1 (GTP binding protein 2)	441	e-123	0
			AAH64968.1	GTPBP2 protein	441	e-123	0
			AAH28347.2	GTPBP2 protein	440	e-123	0
			CAD38999.1	hypothetical protein	427	e-119	0
			NP_061969.2	GTP binding protein 2	424	e-118	0
			BAB12431.1	GTP-binding like protein 2	424	e-118	0
			AAH20980.2	GTPBP2 protein	380	e-105	0

U08378	Mm.24993		ignal transducer and activator of transcription 3 isoform 2;		
1BG1	4	F:2.85	NP_003141.2 acute-phase response factor; DNA-binding protein APRF	1499	0
			AAH00627.1 Signal transducer and activator of transcription 3, isoform 2	1499	0
			signal transducer and activator of transcription 3 isoform 1;		
			NP_644805.1 acute-phase response factor; DNA-binding protein APRF	1494	0
			CAA10032.1 transcription factor	1494	0
			AAH14482.1 Signal transducer and activator of transcription 3, isoform 1	1494	0
			Signal transducer and activator of transcription 3 (Acute-phase		
			response factor)	1485	0
			A54444 DNA-binding protein APRF - human	1485	0
			AAA58374.1 DNA-binding protein	1485	0
			signal transducer and activator of transcription 1 isoform alpha;		
			signal transducer and activator of transcription-1;		
			transcription factor ISGF-3; transcription factor ISGF-3		
			components p91/p84	748	0
			NP_009330.1		
			Signal transducer and activator of transcription 1-alpha/beta		
			(Transcription factor ISGF-3 components p91/p84)	748	0
			P42224		
			transcription factor ISGF-3	748	0
			signal transducer and activator of transcription 1 isoform beta;		
			signal transducer and activator of transcription-1;		
			transcription factor ISGF-3; transcription factor ISGF-3		
			components p91/p84	742	0
			NP_644671.1		
			Signal transducer and activator of transcription 1, isoform beta	742	0
			signal transducer and activator of transcription 1, 91kDa	742	0
			interferon-dependent positive-acting transcription factor ISGF-3 91K		
			chain - human	728	0
			A46159		
			NP_003142.1 signal transducer and activator of transcription 4	674	0
			Q14765 Signal transducer and activator of transcription 4	674	0

AAB05605.1	Signal transducer and activator of transcription 4	674	0
AAH31212.1	STAT4 protein	674	0
1BF5 A	Chain A, Stat-1 Dna Complex	592	e-168
AAL12164.1	signal transducer and activator of transcription 4	568	e-161
	signal transducer and activator of transcription 2; interferon alpha		
NP_005410.1	induced transcriptional activator	478	e-134
P52630	Signal transducer and activator of transcription 2 (p113)	478	e-134
	interferon alpha-induced transcription activator ISGF-3, 113K chain -		
A46160	human	478	e-134
AAA98760.1	Stat2 gene product	478	e-134
AAH51284.1	Signal transducer and activator of transcription 2	478	e-134
NIM_011915			
NP_036045.1	Mm.32831 F:2.83	729	0
AAH18037.1	Wnt inhibitory factor-1	726	0
NP_009122.1	Wnt inhibitory factor-1 precursor; Wnt inhibitory factor-1	726	0
A59180	Wnt inhibitory factor-1	726	0
AAD25402.1	AF122922_1 Wnt inhibitory factor-1	726	0
NIM_009933			
NP_034063.1"	Mm.2509 F:2.81	927	0
NP_001839.1	collagen, type VI, alpha 1 precursor; collagen VI, alpha-1 polypeptide	925	0
P12109	CA16_HUMAN Collagen alpha 1(VI) chain precursor	919	0
CGHU1A	collagen alpha 1(VI) chain precursor	764	0
AAH05159.1	Unknown (protein for IMAGE:3506644)	760	0
CAA67576.1	collagen (VI) alpha-1 chain	754	0
CAA33889.1	alpha-1 collagen VI (AA 574-1009)	728	0
AAH22236.1	Unknown (protein for IMAGE:4178997)	460	e-129
CAA33888.1	precursor polypeptide (AA -19 to 237)	7.00e-	
CGHU2A	collagen alpha 2(VI) chain precursor, long splice form	251	66
	alpha 2 type VI collagen Isoform 2C2 precursor; collagen VI, alpha-2 polypeptide;	7.00e-	
NP_001840.2	human mRNA for collagen VI alpha-2 C-terminal globular domain	251	66

NM_009608 P04270	Mm.686	F:2.81	NP_005150.1	actin, alpha, cardiac muscle precursor	764	0.0
			P04270	ACTC Actin, alpha cardiac	764	0.0
				ATHUC actin, cardiac muscle	764	0.0
			AAB59619.1	alpha-cardiac actin	764	0.0
			AAH09978.1	Actin, alpha, cardiac muscle precursor	764	0.0
			NP_001091.1	alpha 1 actin precursor; alpha skeletal muscle actin	759	0.0
			P02568	ACTS Actin, alpha skeletal muscle	759	0.0
				ATHU actin alpha 1, skeletal muscle	759	0.0
			AAB59376.1	alpha-actin	759	0.0
			AAA60296.1	alpha-skeletal actin precursor	759	0.0
			AAF02694.1	skeletal muscle alpha-actin precursor	759	0.0
			AAH12597.1	Alpha 1 actin precursor	759	0.0
			NP_001604.1	alpha 2 actin; alpha-cardiac actin	755	0.0
			P03996	ACTA Actin, aortic smooth muscle	755	0.0
			CAA32064.1	unnamed protein product	755	0.0
			AAH17554.1	Alpha 2 actin	755	0.0
				ATHUSM actin alpha 2, aortic smooth muscle	752	0.0
			AAA51577.1	alpha-actin	752	0.0
			NP_001606.1	actin, gamma 2 propeptide; actin, alpha-3	750	0.0
			P12718	ACTH Actin, gamma-enteric smooth muscle (Alpha-actin 3)	750	0.0
			A40261	actin gamma, enteric smooth muscle	750	0.0
			CAA34814.1	unnamed protein product	750	0.0
			BAA00546.1	enteric smooth muscle gamma-actin	750	0.0
			AAH12617.1	Actin, gamma 2 propeptide	750	0.0
			NP_001605.1	actin, gamma 1 propeptide; cytoskeletal gamma-actin; actin, cytoplasmic 2	723	0.0
			P02571	ACTG Actin, cytoplasmic 2 (Gamma-actin)	723	0.0
				ATHUG actin gamma 1	723	0.0
			CAA27723.1	amma-actin	723	0.0
			AAA51579.1	gamma-actin	723	0.0

AAH00292.1	Actin, gamma 1 propeptide	723	0.0
AAH01920.1	ACTG1 protein	723	0.0
AAH07442.1	Actin, gamma 1 propeptide	723	0.0
AAH09848.1	Actin, gamma 1 propeptide	723	0.0
AAH10999.1	ACTG1 protein	723	0.0
AAH12050.1	Actin, gamma 1 propeptide	723	0.0
AAH15005.1	ACTG1 protein	723	0.0
AAH15695.1	Actin, gamma 1 propeptide	723	0.0
AAH15779.1	ACTG1 protein	723	0.0
AAH18774.1	ACTG1 protein	723	0.0
AAH53572.1	Actin, gamma 1 propeptide	723	0.0
JC5818	gamma-actin	723	0.0
NP_001092.1	beta actin; beta cytoskeletal actin	722	0.0
P02570	ACTB Actin, cytoplasmic 1 (Beta-actin)	722	0.0
	ATHUB actin beta	722	0.0
CAA25099.1	unnamed protein product	722	0.0
AAA51567.1	cytoplasmic beta actin	722	0.0
AAH01301.1	Beta actin	722	0.0
AAH02409.1	Beta actin	722	0.0
AAH04251.1	Beta actin	722	0.0
AAH13380.1	Beta actin	722	0.0
AAH14861.1	Beta actin	722	0.0
AAP22343.1	unknown	722	0.0
AAH16045.1	Beta actin	720	0.0
CAA45026.1	mutant beta-actin (beta'-actin)	718	0.0
			1.00e-
NM_008546			
NP_032572.1	Mm.7386 F-2.8 NP_002394.1 microfilament-associated protein 2 precursor	288	77
			1.00e-
NP_059453.1	microfilament-associated protein 2 precursor	288	77

NIM_008788	NP_032814.1	Mm.18808	F:2.7	P55001	MFA2_HUMAN Microfibrillar-associated protein 2 precursor (MFAP-2) (Microfibril-associated glycoprotein) (MAGP) (MAGP-1)	288	1.00e-77
				I38923	microfibril-associated glycoprotein MFAP2	288	1.00e-77
				AAA79920.1	microfibril-associated glycoprotein dJ37C10.4 (microfibrillar-associated protein 2 (microfibril-associated glycoprotein precursor, MGAP1))	288	1.00e-77
				CAB96824.1		288	1.00e-77
				AAH15039.1	microfibrillar-associated protein 2 PCO1_HUMAN Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I procollagen COOH-terminal proteinase enhancer) (Type 1 procollagen C-proteinase enhancer protein)	288	1.00e-77
				Q15113	type 1 procollagen C-proteinase enhancer protein	588 e-173	
				BAA23281.1	PCOLCE	588 e-173	
				AAC78800.1	procollagen C-proteinase enhancer protein	588 e-173	
				AAD16041.1	procollagen C-endopeptidase enhancer	588 e-173	
				AAH00574.1	procollagen C-endopeptidase enhancer	588 e-173	
				AAH33205.1	procollagen C-endopeptidase enhancer; procollagen, type 1, COOH-terminal proteinase enhancer	588 e-173	
				NP_002584.1	procollagen I C-proteinase enhancer protein precursor	585 e-172	
				A55362	procollagen C-proteinase enhancer protein	585 e-172	
				AAA61949.1		1.00e-94	
				NP_037495.1	procollagen C-endopeptidase enhancer 2	326	1.00e-94
				AAF04621.1	AF098269_1 procollagen C-terminal proteinase enhancer protein 2	326	1.00e-94
				AAK63128.1	procollagen C-proteinase enhancer protein 2	326	1.00e-94

Accession	Gene	Protein	Length	Score
NM_008438	AAH06265.1	procollagen C-endopeptidase enhancer 2	304	2.00e-82
NP_032464.1	NP_008966.1	keratocan; cornea plana 2 (autosomal recessive)	581	e-165
	O60938	KERA_HUMAN Keratocan precursor (KTN) (Keratan sulfate proteoglycan keratocan)	581	e-165
	AAC16390.1	keratan sulfate proteoglycan	581	e-165
	AAC17741.1	keratocan; kera; corneal keratan sulfate proteoglycan	581	e-165
	AAF69126.1	keratocan	581	e-165
	AAH32667.1	keratocan	581	e-165
	NP_002716.1	proline arginine-rich end leucine-rich repeat protein	339	93
	P51888	PRLP_HUMAN Prolargin precursor (Proline-arginine-rich end leucine-rich repeat protein)	339	93
I39068	I39068	proline- arginine-rich end leucine-rich repeat protein PRELP precursor	339	93
	AAC50230.1	proline- arginine-rich end leucine-rich repeat protein	339	93
	AAC18782.1	prolargin	339	93
AAH32498.1	AAH32498.1	proline arginine-rich end leucine-rich repeat protein	339	93
	AAH35281.1	Similar to fibromodulin	244	64
Q06828	Q06828	FMOD_HUMAN Fibromodulin precursor (FM) (Collagen-binding 59 kDa protein)	241	63
	CAA51418.1	fibromodulin	241	63

NP_002014.1	fibromodulin precursor	237	4.00e-62
S55275	fibromodulin precursor	237	4.00e-62
CAA53233.1	fibromodulin	237	4.00e-62
NP_005005.1	osteomodulin	229	8.00e-60
	OMD_HUMAN Osteomodulin precursor (Osteoadherin) (OSAD) (Keratan sulfate		8.00e-60)
Q99983	proteoglycan osteomodulin) (KSPG osteomodulin)	229	8.00e-60
BAA19055.1	osteomodulin	229	8.00e-60
BAA23982.1	Osteomodulin	229	8.00e-60
AAH46356.1	osteomodulin	229	8.00e-60
AAA85268.1	lumican	227	5.00e-59
NP_002336.1	lumican	227	5.00e-59
	LUM_HUMAN Lumican precursor (Keratan sulfate proteoglycan lumican) (KSPG		5.00e-59)
P51884	lumican)	227	5.00e-59
AAA91639.1	lumican	227	5.00e-59
AAH07038.1	lumican	227	5.00e-59
AAH35997.1	lumican	227	5.00e-59

NM_013651	Mm.26267
NNP_038679	F:2.66 NP_009096.2 Q15428 splicing factor 3a, subunit 2, 66kDa; Spliceosome protein SAP-62 S3A2_HUMAN Splicing factor 3A subunit 2 (Spliceosome associated protein 62) (SAP 62) (SF3a66)
	AAC25613.1 SP62_HUMAN; SAP 62; SF3A66
	AAH04434.1 Splicing factor 3a, subunit 2, 66kDa
	AAH09903.1 Splicing factor 3a, subunit 2, 66kDa
	A47655 spliceosome-associated protein SAP 62
	AAA60301.1 spiceosomal protein
NM_025875	Mm.26197
NNP_080151.1	F:2.65 AAF37551.1 RNA binding motif protein 8
	AAG16781.1 RNA binding motif protein 8A
	NP_005096.1 RNA binding motif protein 8B
	RBM8A_HUMAN RNA-binding protein 8A (RNA binding motif protein 8A)
	(Ribonucleoprotein RBM8A) (RNA-binding protein Y14) (Binder of OVCA1-1) (BOV-1)
	AAD21089.1 ribonucleoprotein RBM8
	AAF29078.1 HSPC114
	AAG27091.1 RNA-binding protein Y14
	AAL26999.1 ribonucleoprotein RBM8
	AAH17088.1 RNA binding motif protein 8A
	AAG14951.1 MDSO14
	AAG16782.1 RNA binding motif protein 8B
	B Chain B, Crystal Structure Of The Human Y14MAGOH COMPLEX
	D Chain D, Crystal Structure Of The Human Y14MAGOH COMPLEX
AK003537	
BAB22844.1	F:2.62 AAB00968.1 microfilament-associated glycoprotein 4
	NP_002395.1 microfilament-associated protein 4; microfibril-associated glycoprotein 4 precursor P55083
	MFE4 HUMAN Microfibril-associated glycoprotein 4 precursor

AAH32953.1	Unknown (protein for MGC:33476)	4.00e-	68
	ficolin 2 isoform a precursor; ficolin (collagen/fibrinogen domain-containing lectin) 2;	256	
NP_004099.1	ficolin (collagen/fibrinogen domain-containing lectin) 2 (hucolin); hucolin	3.00e-	58
	FCN2_HUMAN Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2)	224	
Q15485	(Ficolin-B) (Ficolin B) (Serum lectin p35) (EBP-37) (Huclon) (L-Ficolin)	3.00e-	58
		224	
BAA08352.1	serum lectin P35	3.00e-	58
		224	
BAA09636.1	lectin P35	3.00e-	58
	ficolin 2 isoform b precursor; ficolin (collagen/fibrinogen domain-containing lectin) 2;	224	
NP_056652.1	ficolin (collagen/fibrinogen domain-containing lectin) 2 (huclon); huclon	3.00e-	58
		224	
NP_001994.2	ficolin 1 precursor; ficolin (collagen/fibrinogen domain-containing) 1	2.00e-	56
	FCN1_HUMAN Ficolin 1 precursor (Collagen/fibrinogen domain-containing protein 1)	218	
O00602	(Ficolin-A) (Ficolin A) (M-Ficolin)	2.00e-	56
		218	
AAH20635.1	ficolin (collagen/fibrinogen domain-containing) 1	2.00e-	56
		218	
BAA12120.1	ficolin	2.00e-	56
		218	
S61517	ficolin-1 precursor	1.00e-	55
		215	
AAB50706.1	ficolin	1.00e-	55
	ficolin 3 isoform 1 precursor; ficolin-3; collagen/fibrinogen domain-containing lectin 3	215	
NP_003656.2	p35; collagen/fibrinogen domain-containing protein 3; Hakata antigen; H-ficolin	8.00e-	51
	FCN3_HUMAN Ficolin 3 precursor (Collagen/fibrinogen domain-containing protein 3)	199	
O75636	(Collagen/fibrinogen domain-containing lectin 3 p35) (Hakata antigen)	8.00e-	51
		199	

NM_011340	NP_035470.1	Mm.2044	F:2.62	BAA32277.1	Hakata antigen	199	8.00e-51
					Similar to serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin,		
				AAH00522.1	pigment epithelium derived factor). member 1	659	0
				P36955	PEDF_HUMAN Pigment epithelium-derived factor precursor (PEDF) (EPC-1)	659	0
				AAK92491.1	AF400442_1 pigment epithelium-derived factor	659	0
				A47281	pigment epithelial-differentiating factor precursor	657	0
				AAA60058.1	pigment epithelial-differentiating factor	657	0
				1IMV	A Chain A, 2.85 A Crystal Structure Of Pedf	656	0
				AAH13984.1	Unknown (protein for MGC:20155)	655	0
				A46046	serine proteinase inhibitor homolog EPC-1	603	e-172
NM_011368	2211430A	Mm.86595	F:2.62	NP_002606.1	serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment		
					epithelium derived factor), member 1; pigment epithelium-derived factor	580	e-165
				AAA93524.1	EPC-1 gene product	580	e-165
				AAA84914.1	pigment epithelium-derived factor	545	e-155
				AAB38685.1	EPC-1	501	e-142
					SHC (Src homology 2 domain containing) transforming protein 1; SHC		
				NP_892113.1	(Src homology 2 domain-containing) transforming protein 1	901	0
				P29353	SHC transforming protein	901	0
				AAB49972.1	p66shc	901	0
				CAA70977.1	shc p66	901	0
				S25776	transforming protein (SHC) - human	899	0
				CAA48251.1	SHC transforming protein	899	0
					SHC (Src homology 2 domain containing) transforming protein 1; SHC		
				NP_003020.2	(Src homology 2 domain-containing) transforming protein 1	894	0
				AAH14158.1	SHC (Src homology 2 domain-containing) transforming protein 1	894	0
				AAH33925.1	SHC1 protein	701	0
				BAA12323.1	p52 isoform of N-Shc	487	e-137
				BAA12322.1	p64 isoform of N-Shc	487	e-137

AK011196	NP_058544.2	src homology 2 domain containing transforming protein C3; neuronal	484	e-136
	AAH26314.1	Shc	484	e-136
	P98077	Src homology 2 domain containing transforming protein C3	478	e-134
	BAA25798.1	SCK_HUMAN	478	e-134
	AAH00566.1	Sck	463	e-130
NM_007952	AAH00566.1	Sli, ShcB=53.6 kDa Shc-related protein/Sck homolog [human, fetal brain, Peptide, 486 aa]	320	87
	NP_006851.1	RAYL_HUMAN Putative GTP-binding protein RAY-like (RAB-like protein 4)	313	85
	CAA18787.1	putative GTP-binding protein similar to RAY/RAB1C	313	85
	AAH36000.1	RAB, member of RAS oncogene family-like 4	888	0
	NP_005304.3	hypothetical protein	882	0
NP_031978.1	AAH36000.1	Unknown (protein for IMAGE:4712175)	882	0
	NP_005304.3	glucose regulated protein, 58kDa; glucose regulated protein, 58kD	882	0
	P30101	PDA3_HUMAN Protein disulfide isomerase A3 precursor (Disulfide isomerase ER-60) (ERp60) (58 kDa microsomal protein) (p58) (ERp57) (58 kDa glucose regulated protein)	882	0
	S68363	protein disulfide-isomerase (EC 5.3.4.1) ER60 precursor	882	0
	AAC50331.1	P58	882	0
NP_031978.1	AAH37397.1	H-ERp60=protein disulphide isomerase isoform/multifunctional endoplasmic reticulum luminal polypeptide [human, heart, Peptide, 505 aa]	882	0
	AAH14433.1	Unknown (protein for MGC:2159)	882	0
	2201310A	microsomal protein P58	882	0
	JC5704	protein disulfide-isomerase (EC 5.3.4.1) ER60 precursor	882	0

BAA11928.1	ER-60 protease	882	0
AAC51518.1	ER-60 protein	880	0
S55507	protein disulfide-isomerase (EC 5.3.4.1) ER60 precursor	880	0
CAA89996.1	protein disulfide isomerase	880	0
2209333A	protein disulfide isomerase	880	0
BAA03759.1	phospholipase C-alpha	871	0
S63994	protein disulfide-isomerase (EC 5.3.4.1) ER60 precursor	867	0
2201353A	glucose-regulated protein ERp57/GRP58	863	0
		4.00e-	
NP_004902.1	protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)	340	93
		4.00e-	
P13667	PDA4_HUMAN Protein disulfide isomerase A4 precursor (Protein ERp-72) (ERp72)	340	93
		4.00e-	
A23723	protein disulfide-isomerase (EC 5.3.4.1) ERp72 precursor	340	93
		4.00e-	
AAA58460.1	protein disulfide isomerase-related protein	340	93
		4.00e-	
AAH00425.1	protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)	340	93
		4.00e-	
AAH01928.1	protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)	340	93
		4.00e-	
AAH06344.1	protein disulfide isomerase related protein (calcium-binding protein, intestinal-related) Similar to protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)	340	93
		4.00e-	
AAH11754.1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55); v-erb-a avian erythroblastic leukemia viral oncogene homolog 2-like	340	93
NP_000909.2		250	66
		5.00e-	

					PDI_HUMAN Protein disulfide isomerase precursor (PDI) (Prolyl 4-hydroxylase beta subunit) (Cellular thyroid hormone binding protein) (P55)	5.00e-66
	P07237					250 66
						5.00e-66
	ISHUSS				protein disulfide-isomerase (EC 5.3.4.1) precursor	250 66
						5.00e-66
	AAC13652.1				prolyl 4-hydroxylase beta-subunit	250 66
					procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta	5.00e-66
	AAH10859.1				polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	250 66
					procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta	5.00e-66
	AAH29617.1				polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	250 66
NM_012000		Mm.13253				
NP_036130.1	2	F:2.59			CLN8 protein; epilepsy, progressive with mental retardation	448 e-125
	AAH07725.1				CLN8 protein	448 e-125
					ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	448 e-125
	AAP35698.1					446 e-124
	Q9UBY8				CLN8_HUMAN CLN8 protein	446 e-124
	AAF13117.1				putative transmembrane protein	446 e-124
	AAF13118.1				putative transmembrane protein	446 e-124
	AAF13119.1				putative transmembrane protein	446 e-124
AK008516						
P10076		Mm.9239	F:2.59		zinc finger protein 219	550 e-156
	Q9P2Y4				zinc finger protein 219	550 e-156
	BAA90526.1				zinc finger protein 219	550 e-156
	AAH36105.1				Zinc finger protein 219	550 e-156
	AAH00694.1				Zinc finger protein 219	550 e-156
	AAP35602.1				Zinc finger protein 219	550 e-156
					integral membrane protein 3; E25 protein; BRICHOS domain containing	
NM_022417						
NP_071862.1	Mm.29870	F:2.57			2C	413 e-115
	Q9NQX7				Integral membrane protein 2C (Transmembrane protein BRI3) (NPD018)	413 e-115

NM_007993	AAF89492.1	BRI3	413	e-115
	AAG44792.1	NPD018	413	e-115
	CAB66538.1	hypothetical protein	413	e-115
	AAL15434.1	BRI3	413	e-115
	BAC11570.1	unnamed protein product	413	e-115
	AAH02424.1	Integral membrane protein 3	410	e-114
	BAB46927.1	cerebral protein-14	410	e-114
	CAD28460.1	hypothetical protein	410	e-114
	BAC03562.1	unnamed protein product	397	e-110
	AAH50668.1	ITM2C protein	333	8e-091
NP_032019.1	AAH25742.1	ITM2C protein	315	1e-085
	A47221	fibrillin 1 precursor	5206	0
	P35555	FBN1_HUMAN Fibrillin 1 precursor	5206	0
	AAB02036.1	fibrillin	5206	0
	AAB29419.1	fibrillin [human, Marfan syndrome patient, Peptide Mutant, 2871 aa]	5206	0
	CAA45118.1	fibrillin	5206	0
	1713408A	fibrillin	4217	0
	NP_115823.1	fibrillin 3	3908	0
	BAB47408.1	fibrillin3	3908	0
	AAO18145.1	fibrillin-3 short form precursor transcript variant 1	3907	0
NP_062724.1	AAO18146.1	fibrillin-3 short form precursor transcript variant 2	3907	0
	AAO18147.1	fibrillin-3 short form precursor transcript variant 3	3907	0
	NP_001990.1	fibrillin 2 (congenital contractural arachnodactyly); fibrillin 2	3882	0
	P35556	FBN2_HUMAN Fibrillin 2 precursor	3882	0
	AAA18950.1	fibrillin-2	3882	0
	A54105	fibrillin-2 precursor	3870	0
	1713407B	fibrillin	1224	0
	AAH04483.2	FUS2 protein	326	1e-088
	NM_019750			

Chain B, Crystal Structure Of Human Calcineurin Complexed With Cyclosporin A And Human Cyclophilin			283 2e-076
1MF8 B			283 2e-076
AAB08721.1	calcineurin B		283 2e-076
AAH27913.1	Protein phosphatase 3, regulatory subunit B, alpha isoform 1		283 2e-076
1AUI B	Chain B, Human Calcineurin Heterodimer		
	Chain B, Crystal Structure Of Calcineurin-Cyclophilin-Cyclosporin		
	Shows Common But Distinct Recognition Of		
1M63 B	Immunophilin-Drug Complexes		283 2e-076
	Chain F, Crystal Structure Of Calcineurin-Cyclophilin-Cyclosporin		
	Shows Common But Distinct Recognition Of		
1M63 F	Immunophilin-Drug Complexes		283 2e-076
AAO23957.1	HZGJ		281 7e-076
AAP97278.1	calcineurin B-like protein CBLP		245 5e-065
	protein phosphatase 3 regulatory subunit B, beta isoform; protein phosphatase 3 (formerly 2B), regulatory subunit B (19kD), beta isoform (calcineurin B, type II); calcineurin B, type II; CBLP-like		
NP_671709.1	unnamed protein product		245 5e-065
BAB71521.1	Protein phosphatase 3 regulatory subunit B, beta isoform		245 5e-065
AAH30595.1	CBLP-like protein		243 2e-064
AAP57772.1	CNBI		
AAL40395.1			
NM_019575	Mm.27317		335 1e-091
NP_062521.1	0	F:2.53	335 1e-091
			335 1e-091
			335 1e-091
			335 1e-091
			273 5e-073
			211 3e-054

AAH24700.1	secretory carrier membrane protein 5	211	3e-054
AAM18052.1	secretory carrier membrane protein 5	204	5e-052
CAD38904.1	hypothetical protein		
	RCD1 required for cell differentiation1 homolog; protein involved in sexual development; rcd1 (required for cell differentiation, S.pombe) homolog 1		
NP_005435.1	protein involved in sexual development	564	e-160
BAA13508.1	RQCD1 protein	564	e-160
AAH07102.1		451	e-126
		1237	0
BAA13401.2	Similar to C.elegans hypothetical 37.7 kD protein		
	BRCA1 associated protein-1; cerebra1 protein-13; ubiquitin		
NP_004647.1	carboxy-terminal hydrolase; cerebral protein-6	1233	0
AAC15970.1	BRCA1 associated protein 1	1233	0
AAH01596.1	BRCA1 associated protein 1	1233	0
BAB46921.1	cerebral protein-6	1233	0
AAN05092.1	MU-MB-17.261	939	0
	potassium voltage-gated channel, subfamily H, member 7 isoform 1; potassium channel subunit HERG-3; ether-a-go-go related gene potassium channel 3; eag related protein 3	2123	0
NP_150375.2	KCH7_HUMAN Potassium voltage-gated channel subfamily H member 7		
	(Ether-a-go-go related gene potassium channel 3) (HERG-3) (Ether-a-go-go related protein 3) (Eag related protein 3)	2105	0
Q9NS40	potassium channel subunit	2105	0
AAD01946.1	potassium voltage-gated channel, subfamily H, member 7 isoform 2; potassium channel subunit HERG-3; ether-a-go-go related gene potassium channel 3; eag related protein 3		
NP_775185.1	related protein 3	1346	0
AAH35815.1	Similar to potassium voltage-gated channel, subfamily H (eag-related), member 7	1346	0
AAN05415.1	ether-a-go-go related potassium channel	1128	0

NP_000229.1	voltage-gated potassium channel, subfamily H, member 2 isoform a; potassium voltage-gated channel, subfamily H, member 2; ether-a-go-go-related potassium channel protein; human eag-related gene	1125	0
KCH2_HUMAN	Potassium voltage-gated channel subfamily H member 2 (Ether-a-go-go related gene potassium channel 1) (H-ERG) (Erg1) (Ether-a-go-go related protein 1) (Eag related protein 1) (eag homolog)	1125	0
Q12809	probable potassium channel subunit	1125	0
I38465	putative potassium channel subunit	1125	0
AAA62473.1	a gene responsible for familial long QT syndrome (LQT2)	1125	0
BAA37096.1	AF363636_1 ether-a-go-go-related K+ channel protein	1125	0
AAL37559.1	ether-a-go-go-related protein	1076	0
CAA09232.1	voltage-gated potassium channel, subfamily H, member 2 isoform b; potassium voltage-gated channel, subfamily H, member 2; ether-a-go-go-related potassium channel protein; human eag-related gene	1003	0
NP_742053.1	HERG-USO	1001	0
BAB19682.1	Similar to potassium voltage-gated channel, subfamily H (eag-related), member 2 potassium voltage-gated channel, subfamily H, member 6 isoform 1; eag-related gene member 2; ether-a-go-go related gene potassium channel 2; eag related protein 2	875	0
AAH01914.1	KCH6_HUMAN Potassium voltage-gated channel subfamily H member 6 (Ether-a-go-go related gene potassium channel 2) (Ether-a-go-go related protein 2)	851	0
NP_110406.1	(Eag related protein 2)	851	0
Q9H252	AF311913_1 Eag-related gene member 2	851	0
AAG40871.1	block of proliferation 1	1174	0
NM_013481	Block of proliferation 1	1174	0
NP_056016.1	Block of proliferation 1	1174	0
Q14137	Block of proliferation 1	1174	0
AAH13787.1	Block of proliferation 1	1174	0
AAH13980.1	Block of proliferation 1	1174	0
AAH17674.1	Block of proliferation 1	1174	0

	AAH07274.1	Similar to block of proliferation 1	1171	0
	AAH05160.2	BOP1 protein	1166	0
	BAA09473.1	The KIAA0124 gene product is novel.	1159	0
	AAH01086.2	BOP1 protein	1154	0
	BAB70666.1	KM-PA-2 protein	1128	0
AK004884				
NP_150289.1	Q9Y2K5	Hypothetical protein KIAA1002	1145	0
	BAA76846.2	KIAA1002 protein	1145	0
	NP_055740.2	KIAA1002 protein	1080	0
	Q15032	R3H domain protein 1	539	e-152
	BAA04878.2	KIAA0029	539	e-152
	NP_056176.2	R3H domain (binds single-stranded nucleic acids) containing	455	e-127
	AAH41093.1	R3H domain (binds single-stranded nucleic acids) containing	455	e-127
AK006635				
JC5583	Mm.26144	hypothetical protein	458	0
	F:2.49	Rac/Cdc42 guanine nucleotide exchange factor 6; PAK-interacting exchange factor, alpha; Rac/Cdc42 guanine exchange factor 6 (GEF) 6; rho guanine nucleotide exchange factor 6	458	0
	NP_004831.1	Rho guanine nucleotide exchange factor 6 (PAK-Interacting exchange factor alpha) (Alpha-Pix) (COOL-2)	458	0
	Q15052	Rac/Cdc42 guanine nucleotide exchange factor 6	458	0
	AAH39856.1	KIAA0006	458	0
	BAA04985.1	ARHGEF6 protein	458	0
	AAH43505.1	KIAA0006	458	0
	BAA02796.1	hypothetical protein	458	e-171
	CAD38906.1	ARHGEF7 protein	305	e-163
	AAH60776.1	KIAA0142	338	e-111
	BAA09763.2		338	e-111

NM_009075	P47968	Mm.17905	F:2.48	NP_663788.1	Rho guanine nucleotide exchange factor 7 isoform b; SH3 domain-containing proline-rich protein; PAK-interacting exchange factor beta	338	e-111
				AAH50521.1	Rho guanine nucleotide exchange factor (GEF) 7	338	e-111
NM_007788	P47968	Mm.17905	F:2.48	NP_653164.1	ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase); RIBOSE 5-PHOSPHATE ISOMERASE	450	e-126
				P49247	Ribose 5-phosphate isomerase (Phosphoriboisomerase)	450	e-126
				AAK95569.1	ribose 5-phosphate isomerase	450	e-126
				NP_001886.1	casein kinase II alpha 1 subunit isoform a; CK2 catalytic subunit alpha	730	0
NM_007788	P47968	Mm.23692	F:2.48	NP_808227.1	casein kinase II alpha 1 subunit isoform a; CK2 catalytic subunit alpha	730	0
				P19138	Casein kinase II, alpha chain (CK II)	730	0
				A30319	casein kinase II (EC 2.7.1.-) alpha chain - human	730	0
				AAA35503.1	casein kinase II alpha subunit	730	0
				AAA56821.1	casein kinase II alpha subunit	730	0
				CAB65624.1	dJ863C7.1.1 (casein kinase 2, alpha 1 polypeptide (EC 2.7.1.37))	730	0
				AAH11668.1	Casein kinase II alpha 1 subunit, isoform a	730	0
				AAH53532.1	Casein kinase II alpha 1 subunit, isoform a	730	0
				CAA49758.1	casein kinase II alpha subunit	722	0
				AAM52224.1	casein kinase II alpha subunit	719	0
				1JWHIA	Chain A, Crystal Structure Of Human Protein Kinase Ck2 Holoenzyme	652	0
				1JWHIB	Chain B, Crystal Structure Of Human Protein Kinase Ck2 Holoenzyme	652	0
				1PJKIA	Chain A, Crystal Structure Of A C-Terminal Deletion Mutant Of Human Protein Kinase Ck2 Catalytic Subunit	648	0
				1NA7IA	Chain A, Crystal Structure Of The Catalytic Subunit Of Human Protein Kinase Ck2 Catalytic Subunit	638	0
				NP_001887.1	casein kinase 2, alpha prime polypeptide	558	e-158
				P19784	Casein kinase II, alpha' chain (CK II)	558	e-158
				B35838	casein kinase II (EC 2.7.1.-) alpha' chain - human	558	e-158

	AAA51548.1	casein kinase II alpha' subunit	558	e-158
	AAH08812.1	Casein kinase 2, alpha prime polypeptide	558	e-158
	NP_808228.1	casein kinase II alpha 1 subunit isoform b; CK2 catalytic subunit alpha	500	e-141
		flotillin 2; Flotillin 2 (epidermal surface antigen 1); membrane component, chromosome 17, surface marker 1 (35kD protein identified by monoclonal antibody ECS-1)	659	0
NM_008028	NP_004466.1	Flotillin-2 (Epidermal surface antigen) (ESA)	659	0
O08917	Q14254	epidermal surface antigen - human	659	0
	A53664	surface antigen	659	0
	AAH65729.1	Flotillin 2	659	0
	AAH17292.1	Similar to flotillin 2	659	0
	AAH03683.1	flotillin	574	e-163
	AAD40192.1	flotillin 1	337	8e-092
	NP_005794.1	flotillin 1	336	1e-091
	O75955	flotillin 1	336	1e-091
	AAC35387.1	flotillin 1	336	1e-091
	AAH01146.1	flotillin 1	336	1e-091
	BAB63320.1	alternative name: FLOTILLIN	336	1e-091
	BAC54934.1	flotillin 1	336	1e-091
	AAP35740.1	flotillin 1	336	1e-091
	AAF17215.1	flotillin	208	4e-053
NM_016670		PBX/knotted 1 homeobox 1 isoform 1; human homeobox-containing protein; Pbx regulating protein-1	731	0
O70477	NP_004562.2	PBX/knotted 1 homeobox 1, isoform 1	731	0
	AAH07746.1	homeobox-containing protein PKNOX1	731	0
	AAO45825.1	Homeobox protein PKNOX1 (PBX/knotted homeobox 1) (Homeobox protein PREP-1)	729	0
	P55347	homeobox-containing protein	729	0
	BAA95533.1	Prep-1	727	0
	CAA73934.1			

AAC51243.1	homeobox-containing protein PBX/knotted 1 homeobox 1 isoform 2; human homeobox-containing	726	0
NP_932080.1	protein; Pbx regulating protein-1	633	0
AAN34940.1	PKNOX1B	633	0
AAH00735.1	PKNOX1 protein	576	e-164
AAH45626.2	PKNOX2 protein	425	e-118
	Homeobox protein PKNOX2 (PBX/knotted homeobox 2) (Homeobox protein		
Q96KN3	PREP-2)	424	e-118
CAD01142.1	PREP2 protein	424	e-118
BAB83665.1	PKNOX2	424	e-118
	three-amino-acid loop extension(TALE) homeodomain protein, PKNOX2 -		
JC7766	human	423	e-117
NP_071345.1	PBX/knotted 1 homeobox 2	281	8e-075
BAB14422.1	unnamed protein product	281	8e-075
NIM_008686			
I48694			
BAC03440.1	FLJ00380 protein	1294	0
A49672	transcription factor Nrf1 - human	1285	0
AAH10623.1	NFE2L1 protein	1285	0
	nuclear factor (erythroid-derived 2)-like 1; transcription factor 11		
NP_003195.1	(basic leucine zipper type)	1269	0
	Nuclear factor erythroid 2 related factor 1 (NF-E2 related factor 1)		
	(NFE2-related factor 1) (Nuclear factor, erythroid		
	derived 2, like 1) (Transcription factor 11)		
	(Transcription factor HBZ17) (Transcription factor		
Q14494	LCR-F1) (Locus control region-factor 1)	1269	0
A55004	transcription factor TFC11 - human	1269	0
CAA54555.1	hbZ17	1269	0
AAA20466.1	transcription factor LCR-F1	724	0
NP_004280.3	nuclear factor (erythroid-derived 2)-like 3; NF-E2-related factor 3	299	3e-080

NM_016857	T03722	Mm.22530 F:2.45	AAF61404.1	NF-E2-related factor 3	299	3e-080
			AAF61415.1	NF-E2-related factor 3	299	3e-080
			AAG43275.1	NF-E2-related factor 3	299	3e-080
			AAH56142.1	NFE2L3 protein	251	9e-066
			AAH49219.1	NFE2L3 protein	242	4e-063
			BAA76288.1	NF-E2-related factor 3	242	4e-063
			AAP22344.1	UNKNOWN	242	4e-063
			NP_006155.2	nuclear factor (erythroid-derived 2)-like 2	241	7e-063
				Nuclear factor erythroid 2 related factor 2 (NF-E2 related factor 2)		
				(NFE2-related factor 2) (Nuclear factor, erythroid		
NM_016857	T03722	Mm.22530 F:2.45	Q16236	derived 2, like 2) (HEBP1)	241	7e-063
			AAH11558.1	Nuclear factor (erythroid-derived 2)-like 2	241	7e-063
			AAF17228.1	NFE2-related factor 1	236	2e-061
			BAA83019.1	KIAA1067 protein	1231	0
			CAD38992.1	hypothetical protein	1231	0
			AAH11045.1	EXOC7 protein	1231	0
			Q9UPT5	Exocyst complex component Exo70	1207	0
			AAH18466.1	EXOC7 protein	1204	0
			NP_056034.1	exocyst complex component 7	1146	0
BC016102	AAH16102.1	Mm.20420 F:2.45	BAB14694.1	unnamed protein product	1146	0
			BAB14095.1	unnamed protein product	478	e-134
			BAB14026.1	unnamed protein product	478	e-134
				DNA-directed RNA polymerase III 47 kDa polypeptide (RNA polymerase C		
			P05423	subunit 4) (RPC4) (RPC53) (BN51 protein)	582	e-165
			AAH02603.1	POLR3D protein	582	e-165
			AAH04484.1	POLR3D protein	582	e-165
			AAM18216.1	RNA polymerase III 53 kDa subunit RPC4	578	e-164

RNA polymerase III 53 kDa subunit RPC4; temperature sensitive complementation, cell cycle specific, tsBN51; BN51				
NP_001713.1	(BHK21) temperature sensitivity complementing		558	e-158
A43700	BN51 protein - human		558	e-158
AAA51838.1	BN51 protein		558	e-158
AAH03039.1	POLR3D protein		219	2e-067
NM_009926				
NP_034056.1	Mm.20230 F:2.44	alpha 2 type XI collagen isoform 2 preproprotein	1099	0
AAC50213.1	Pro-a2(XI)		1092	0
NP_542410.1	alpha 2 type XI collagen isoform 3 preproprotein		1058	0
AAC50215.1	Pro-a2(XI)		1052	0
NP_542411.1	alpha 2 type XI collagen isoform 1 preproprotein		998	0
P13942	CA2B_HUMAN Collagen alpha 2(XI) chain precursor		997	0
CAA20240.1	dJ1033B10.12 (collagen, type XI, alpha 2)		996	0
CGHU2E	collagen alpha 2(XI) chain precursor		994	0
AAC50214.1	Pro-a2(XI)		991	0
2123363A	collagen:SUBUNIT=alpha2:ISOTYPE=XI		991	0
AAA35498.1	alpha-2 type XI collagen		811	0
1917210A	Pro/Arg-rich protein (alpha-2 type XI collagen)		811	0
NM_018862				
O35083	Mm.8684 F:2.44	1-acylglycerol-3-phosphate O-acyltransferase 1; lysophosphatidic acid acyltransferase	496	e-140
NP_006402.1	alpha; 1-AGP acyltransferase 1; lysophospholipid acyltransferase			
NP_116130.2	1-acylglycerol-3-phosphate O-acyltransferase 1; lysophosphatidic acid acyltransferase		496	e-140
	alpha; 1-AGP acyltransferase 1; lysophospholipid acyltransferase			
	PLCA_HUMAN 1-acyl-sn-glycerol-3-phosphate acyltransferase alpha (1-AGP acyltransferase 1) (1-AGPAT 1) (Lysophosphatidic acid acyltransferase-alpha)			
Q99943	(LPAAT-alpha) (1-acylglycerol-3-phosphate O-acyltransferase 1) (G15 protein)		496	e-140
AAB58775.1	lysophosphatidic acid acyltransferase-alpha		496	e-140
AAB96378.1	putative lysophospholipid acyltransferase		496	e-140
CAA70758.1	1-acylglycerol-3-phosphate O-acyltransferase		496	e-140

AAH02402.1	1-acylglycerol-3-phosphate O-acyltransferase 1	496	e-140
AAH03007.1	1-acylglycerol-3-phosphate O-acyltransferase 1	496	e-140
AAH04310.1	1-acylglycerol-3-phosphate O-acyltransferase 1	496	e-140
AAB47493.1	LPAAT	487	e-137
AAC19153.1	unknown	458	e-128
AAG17276.1	unknown	325	2e-088
AAB64299.1	lysophosphatidic acid acyltransferase	235	2e-061
	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid		
AAH19292.1	acyltransferase, beta)	234	3e-061
	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid		
	acyltransferase, beta); lysophosphatidic acid acyltransferase beta; Berardinelli-Seip		
NP_006403.2	congenital lipodystrophy	234	3e-061
	PLCB_HUMAN 1-acyl-sn-glycerol-3-phosphate acyltransferase beta (1-AGP		
	acyltransferase 2) (1-AGPAT 2) (Lysophosphatidic acid acyltransferase-beta)		
O15120	(LPAAT-beta) (1-acylglycerol-3-phosphate O-acyltransferase 2)	234	3e-061
AAC51649.1	lysophosphatidic acid acyltransferase	234	3e-061
AAB58776.2	lysophosphatidic acid acyltransferase-beta	234	3e-061
	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid		
AAH00026.1	acyltransferase, beta)	233	7e-061
	mitogen-activated protein kinase kinase 7; dual specificity		
	mitogen-activated protein kinase kinase 7; c-Jun		
	N-terminal kinase kinase 2; MAP kinase kinase 7;		
NM_011944	JNK-activating kinase 2; JNK kinase 2	710	0
NP_036074	Dual specificity mitogen-activated protein kinase kinase 7 (MAP		
	kinase kinase 7) (MAPKK 7) (MAPK/ERK kinase 7) (JNK		
	activating kinase 2) (c-Jun N-terminal kinase kinase 2)		
O14733	(JNK kinase 2) (JNKK 2)	710	0
AAC26142.1	c-Jun N-terminal kinase kinase 2	710	0

AAC16272.1	mitogen-activated protein kinase kinase 7	708	0
AAB88048.1	JNK kinase 2	708	0
AAH38295.1	MAP2K7 protein	703	0
AAC16273.1	mitogen-activated protein kinase kinase 7b	687	0
AAB97813.1	Jnkk2	675	0
AAB63374.1	MAP kinase kinase 7	393	e-109
AAH36032.1	Mitogen-activated protein kinase kinase 4	290	7e-078
	mitogen-activated protein kinase kinase 4; dual specificity		
	mitogen-activated protein kinase kinase 4; MAP kinase		
	kinase 4; c-Jun N-terminal kinase kinase 1; JNK		
	activating kinase 1; SAPK/ERK kinase 1; MAPK/ERK kinase		
NP_003001.1	4; JNK-activated kinase 1	290	7e-078
	Dual specificity mitogen-activated protein kinase kinase 4 (MAP		
	kinase kinase 4) (JNK activating kinase 1) (c-Jun		
	N-terminal kinase kinase 1) (JNKK) (SAPK/ERK kinase 1)		
P45985	(SEK1)	290	7e-078
I38901	JNK-activating protein kinase (EC 2.7.1.-) - human	290	7e-078
AAC41719.1	MAP kinase kinase 4	290	7e-078
AAC50127.1	JNK activating kinase	290	7e-078
AAC24130.1	mitogen-activated protein kinase kinase 1	290	7e-078
AAH60764.1	Mitogen-activated protein kinase kinase 4	286	1e-076
NM_011305			
P28700			
Mm.3470	F-2.44	848	0
AAH63827.1	RXRA protein	833	0
NP_002948.1	retinoid X receptor, alpha	833	0
P19793	Retinoic acid receptor RXR-alpha	833	0
S09592	retinoid X receptor alpha [validated] - human	833	0
CAA36982.1	unnamed protein product	833	0
1609194A	retinoic acid receptor RXRalpha	833	0

NP_008848.1	retinoid X receptor, gamma	590	e-168
P48443	Retinoic acid receptor RXR-gamma	590	e-168
AAA80681.1	retinoid X receptor-gamma	590	e-168
CAC00596.1	bA280O1.2 (retinoid X receptor, gamma (NR2B3))	590	e-168
AAH12063.1	Retinoid X receptor, gamma	590	e-168
AAA60293.1	retinoid X receptor beta	574	e-163
NP_068811.1	retinoid X receptor, beta; MHC class I promoter binding protein	574	e-163
P28702	Retinoic acid receptor RXR-beta	574	e-163
CAA45087.1	retinoic acid X receptor b	574	e-163
AAC18599.1	retinoic X receptor B	574	e-163
CAA20239.1	dJ1033B10.11 (retinoid X receptor beta)	574	e-163
AAD13794.1	retinoic X receptor beta	574	e-163
AAH01167.1	Retinoid X receptor, beta	574	e-163
AAP35944.1	Retinoid X receptor, beta	574	e-163
S37781	retinoid X receptor beta - human	574	e-163
1LBD	Ligand-Binding Domain Of The Human Nuclear Receptor Rxr-Alpha	518	e-146
	Chain A, Crystal Structure Of The Human Rxr Alpha Ligand Binding		
	Domain Bound To The Eicosanoid Dha (Docosa Hexaenoic		
	Acid) And A Coactivator Peptide	476	e-134
1MV9 A	Chain A, Crystal Structure Of The Human Rxr Alpha Ligand Binding		
	Domain Bound To The Synthetic Agonist Compound Bms 649		
	And A Coactivator Peptide	476	e-134
1MVC A	Chain A, Crystal Structure At 1.9 Angstroms Resolution Of The		
	Homodimer Of Human Rxr Alpha Ligand Binding Domain Bound		
	To The Synthetic Agonist Compound Bms 649 And A		
	Coactivator Peptide	476	e-134
1MZN A			

1MZN C	Chain C, Crystal Structure At 1.9 Angstroms Resolution Of The Homodimer Of Human Rxr Alpha Ligand Binding Domain Bound To The Synthetic Agonist Compound Bms 649 And A Coactivator Peptide	476 e-134
1MZN E	Chain E, Crystal Structure At 1.9 Angstroms Resolution Of The Homodimer Of Human Rxr Alpha Ligand Binding Domain Bound To The Synthetic Agonist Compound Bms 649 And A Coactivator Peptide	476 e-134
1MZN G	Chain G, Crystal Structure At 1.9 Angstroms Resolution Of The Homodimer Of Human Rxr Alpha Ligand Binding Domain Bound To The Synthetic Agonist Compound Bms 649 And A Coactivator Peptide	476 e-134
1FBY A	Chain A, Crystal Structure Of The Human Rxr Alpha Ligand Binding Domain Bound To 9-Cis Retinoic Acid	474 e-133
1FBY B	Chain B, Crystal Structure Of The Human Rxr Alpha Ligand Binding Domain Bound To 9-Cis Retinoic Acid	474 e-133
1FM6 A	Chain A, The 2.1 Angstrom Resolution Crystal Structure Of The Heterodimer Of The Human Rxralpha And Ppargamma Ligand Binding Domains Respectively Bound With 9-Cis Retinoic Acid And Rosiglitazone And Co-Activator Peptides.	473 e-133
1FM6 U	Chain U, The 2.1 Angstrom Resolution Crystal Structure Of The Heterodimer Of The Human Rxralpha And Ppargamma Ligand Binding Domains Respectively Bound With 9-Cis Retinoic Acid And Rosiglitazone And Co-Activator Peptides.	473 e-133

1FM9 A	Chain A, The 2.1 Angstrom Resolution Crystal Structure Of The Heterodimer Of The Human Rxralpha And Ppargamma Ligand Binding Domains Respectively Bound With 9-Cis Retinoic Acid And Gi262570 And Co-Activator Peptides.	473 e-133
1G5Y A	Chain A, The 2.0 Angstrom Resolution Crystal Structure Of The Rxralpha Ligand Binding Domain Tetramer In The Presence Of A Non-Activating Retinoic Acid Isomer.	473 e-133
1G5Y B	Chain B, The 2.0 Angstrom Resolution Crystal Structure Of The Rxralpha Ligand Binding Domain Tetramer In The Presence Of A Non-Activating Retinoic Acid Isomer.	473 e-133
1G5Y C	Chain C, The 2.0 Angstrom Resolution Crystal Structure Of The Rxralpha Ligand Binding Domain Tetramer In The Presence Of A Non-Activating Retinoic Acid Isomer.	473 e-133
1G5Y D	Chain D, The 2.0 Angstrom Resolution Crystal Structure Of The Rxralpha Ligand Binding Domain Tetramer In The Presence Of A Non-Activating Retinoic Acid Isomer.	473 e-133
1G1U A	Chain A, The 2.5 Angstrom Resolution Crystal Structure Of The Rxralpha Ligand Binding Domain In Tetramer In The Absence Of Ligand	473 e-133
1G1U B	Chain B, The 2.5 Angstrom Resolution Crystal Structure Of The Rxralpha Ligand Binding Domain In Tetramer In The Absence Of Ligand	473 e-133
1G1U C	Chain C, The 2.5 Angstrom Resolution Crystal Structure Of The Rxralpha Ligand Binding Domain In Tetramer In The Absence Of Ligand	473 e-133

NM_008995 O09012	1G1U D	Chain D, The 2.5 Angstrom Resolution Crystal Structure Of The Rxlpha Ligand Binding Domain In Tetramer In The Absence Of Ligand		473	e-133
		Chain A, The 2.3 Angstrom Resolution Crystal Structure Of The Heterodimer Of The Human Ppargamma And Rxlpha Ligand Binding Domains Respectively Bound With Gw409544 And 9-Cis Retinoic Acid And Co-Activator Peptides.		473	e-133
NM_008995 O09012	1K74 A	A56126 peroxisomal targeting signal 1 receptor - human		1107	0
		CAA59324.1 peroxisomal C-terminal targeting signal import receptor		1107	0
NM_008995 O09012	1K74 A	NP_000310.2 peroxisome receptor 1		1082	0
		AAH10621.1 peroxisome receptor 1		1082	0
NM_008995 O09012	1K74 A	Peroxisomal targeting signal 1 receptor (Peroxisome receptor 1) (Peroxisomal C-terminal targeting signal import receptor)		1055	0
		P50542 (PTS1-BP) (Peroxin-5) (PTS1 receptor)		1055	0
NM_008995 O09012	1K74 A	CAA88131.1 peroxisomal targeting signal 1 (SKL type) receptor		1053	0
		AAC50103.1 peroxisomal targeting signal receptor 1		1053	0
NM_008995 O09012	1FCH A	Chain A, Crystal Structure Of The Pts1 Complexed To The Tpr Region Of Human Pex5		655	0
		Chain B, Crystal Structure Of The Pts1 Complexed To The Tpr Region Of Human Pex5		655	0
NM_008995 O09012	1FCH B	BAA92878.1 PXR2a		376	e-104
		NP_057643.1 PXR2b protein		376	e-104
NM_008995 O09012	1FCH B	BAA92879.1 PXR2b		376	e-104
		AAH36183.1 PEX5R protein		373	e-103
NM_008995 O09012	1FCH B	Q99943 PEX5 related protein		342	1e-093
		AAC50344.1 peroxisomal targeting signal import receptor		217	5e-056

P11082	Mm.3294	F:2.42	NP_006238.1	protein phosphatase 5, catalytic subunit Serine/threonine protein phosphatase 5 (PP5) (Protein phosphatase T)	958	0
			P53041	(PP-T) (PPT)	958	0
			AAD22669.1	PPP5_HUMAN	958	0
			AAH01970.1	PPP5C protein	958	0
			AAP35939.1	protein phosphatase 5, catalytic subunit	958	0
			CAA61595.1	protein phosphatase 5	947	0
			AAB60384.1	serine-threonine phosphatase	942	0
			S52570	phosphoprotein phosphatase (EC 3.1.3.16) 5 [validated] - human	940	0
			AAH00750.4	PPP5C protein	928	0
			AAH01831.4	PPP5C protein	928	0
			1A17	Tetratricopeptide Repeats Of Protein Phosphatase 5 serine/threonine protein phosphatase with EF-hand motifs 1 isoform 1b; protein phosphatase, serine/threonine type, with EF-hands; serine/threonine protein phosphatase 7	328	3e-089
			NP_689410.1	phosphatase 2A	231	3e-060
			AAB38020.1	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	223	1e-057
			NP_004147.1	Serine/threonine protein phosphatase 2A, catalytic subunit, beta isoform (PP2A-beta)	221	4e-057
			P11082	phosphoprotein phosphatase (EC 3.1.3.16) 2-beta catalytic chain - human	221	4e-057
			PAHU2B	unnamed protein product	221	4e-057
			CAA31183.1	protein phosphatase-2A catalytic subunit-beta	221	4e-057
			AAA36467.1	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	221	4e-057
			AAH12022.1	protein phosphatase type 2A catalytic subunit	221	4e-057
			AAL35904.1	aquaporin 4 isoform a; mercurial-insensitive water channel	521	e-148
U33012	Mm.25078				521	e-148
P55088	6	F:2.42	NP_001641.1	Aquaporin 4 (WCH4) (Mercurial-insensitive water channel) (MIWC)	521	e-148
			P55087		521	e-148

BAA09715.1	aquaporin	521	e-148
AAB26957.1	aquaporin 4	521	e-148
AAH22286.1	Aquaporin 4, isoform a	521	e-148
I39178	aquaporin 4, long splice form - human	516	e-146
AAC52112.1	mercurial-insensitive water channel	516	e-146
NP_004019.1	aquaporin 4 isoform b; mercurial-insensitive water channel	505	e-143
AAB26958.1	aquaporin 4	505	e-143
AAC50284.1	mercurial-insensitive water channel	500	e-141
NP_001642.1	aquaporin 5; Aquaporin-5	221	2e-057
P55064	Aquaporin 5	-221	2e-057
AAC50474.1	aquaporin-5	221	2e-057
AAH32946.1	aquaporin-5	221	2e-057
NP_036196.1	major intrinsic protein of lens fiber; aquaporin	215	1e-055
P30301	Lens fiber major intrinsic protein (MIP26) (MP26) (Aquaporin 0)	215	1e-055
A55279	major intrinsic protein - human	215	1e-055
AAC02794.2	lens major intrinsic protein	215	1e-055
AAB30268.1	hAQP-CD=collecting duct aquaporin [human, kidney, Peptide, 271 aa]	215	1e-055
NP_000477.1	aquaporin 2; collecting duct water channel protein; aquaporin-CD	215	1e-055
	Aquaporin-CD (AQP-CD) (Water channel protein for renal collecting duct) (ADH water channel) (Aquaporin 2) (Collecting duct	214	2e-055
P41181	water channel protein) (WCH-CD)	214	2e-055
A53442	aquaporin 2 - human	214	2e-055
CAA82627.1	water channel aquaporin-2	214	2e-055
BAA06632.1	human aquaporin-2 water channel	214	2e-055
AAD38692.1	aquaporin 2	214	2e-055
AAH42496.1	aquaporin 2	214	2e-055
I52366	uterine water channel - human	212	9e-055
AAB31193.1	uterine water channel; hUWC	212	9e-055
AAL87136.1	aquaporin 1	211	1e-054

NM_013868				heat shock 27kDa protein family, member 7 (cardiovascular);			
P35385	Mm.46181	F:2.41	NP_055239.1	cardiovascular heat shock protein; heat shock 27kD protein family, member 7 (cardiovascular)		274 7e-073	
			Q9UBY9	HSB7_HUMAN Heat-shock protein, beta-7 (Cardiovascular heat shock protein) (cvHsp)		274 7e-073	
			CAB63258.1	heat shock protein		274 7e-073	
			AAF20022.1	cardiovascular heat shock protein		274 7e-073	
			AAH06319.1	Heat shock 27kDa protein family, member 7 (cardiovascular)		274 7e-073	
			CAD97949.1	hypothetical protein		271 3e-072	
			CAB86671.1	dJ336M4.5 (cardiovascular heat shock protein)		270 7e-072	
			BAC03846.1	unnamed protein product		263 1e-069	
				43 kD receptor-associated protein of the synapse isoform 1; rapsyn;			
NM_009023				acetylcholine receptor-associated 43 kda protein; 43 kda			
P12672	Mm.1272	F:2.4	NP_005046.2	postsynaptic protein		806 0	
			AAL86639.1	43kDa acetylcholine receptor-associated protein		806 0	
				43 kDa receptor-associated protein of the synapse (RAPSYN)			
				(Acetylcholine receptor-associated 43 kDa protein) (43			
			Q13702	kDa postsynaptic protein)		805 0	
			S45064	nicotinic acetylcholine receptor-associated 43K protein - human		803 0	
			CAA83954.1	43kD Acetylcholine receptor-associated protein (Rapsyn)		803 0	
				43 kD receptor-associated protein of the synapse isoform 2; rapsyn;			
				acetylcholine receptor-associated 43 kda protein; 43 kda			
			NP_116034.2	postsynaptic protein		621 e-177	
			AAH04196.1	43 kD receptor-associated protein of the synapse, isoform 2		619 e-177	
NM_023637	Mm.27518						
NP_076126	3	F:2.4	NP_060297.1	seryl-tRNA synthetase 2; serine-tRNA ligase, mitochondrial		852 0	
				Seryl-tRNA synthetase, mitochondrial precursor (Serine--tRNA ligase)			
			Q9NP81	(SerRSmt)		852 0	

NIM_009179	Mm.20038		BAA91176.1	unnamed protein product	852	0
A54420	8	F:2.38	BAA99557.1	mitochondrial seryl-tRNA synthetase	852	0
			AAH42912.1	Seryl-tRNA synthetase 2	852	0
			AAH01020.2	SARS2 protein	268	3e-071
				sialyltransferase 4B; sialyltransferase 4B (beta-galactoside alpha-2,3-sialyltransferase); alpha 2,3-ST; Gal-beta-1,3-GalNAc-alpha-2,3-sialyltransferase; CMP-N-acetylneuraminatate-beta-galactosamide-alpha-2, 3-sialyltransferase	702	0
				CMP-N-acetylneuraminatate-beta-galactosamide-alpha-2, 3-sialyltransferase (Beta-galactoside alpha-2,3-sialyltransferase) (Alpha 2,3-ST) (Gal-NAc6S) (Gal-beta-1,3-GalNAc-alpha-2,3-sialyltransferase) (ST3GalA.2) (SIAT4-B) (ST3Gal II)	702	0
			Q16842	beta-galactoside alpha-2,3-sialyltransferase (EC 2.4.99.4) - human	702	0
			JC5251	beta-galactoside alpha-2,3-sialyltransferase	702	0
			CAA65447.1	Gal beta-1,3 GalNAc alpha-2,3 sialyltransferase	702	0
			AAB40389.1	Sialyltransferase 4B	702	0
			AAH36777.1	sialyltransferase 4A;	702	0
				CMP-N-acetylneuraminatate-beta-galactosamide-alpha-2, 3-sialyltransferase; sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase); alpha 2,3-ST; Gal-beta-1,3-GalNAc-alpha-2,3-sialyltransferase sialyltransferase 4A;	357	3e-098
			NP_003024.1	CMP-N-acetylneuraminatate-beta-galactosamide-alpha-2, 3-sialyltransferase; sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase); alpha 2,3-ST; Gal-beta-1,3-GalNAc-alpha-2,3-sialyltransferase	357	3e-098
			NP_775479.1			

NM_016973	CMP-N-acetylneuraminase-beta-galactosaminide-alpha-2,		
	3-sialyltransferase (Beta-galactoside		
	alpha-2,3-sialyltransferase) (Alpha 2,3-ST) (Gal-NAc6S)		
	(Gal-beta-1,3-GalNAc-alpha-2,3-sialyltransferase)		
	(ST3GalIA) (ST3O) (ST3GalA.1) (SIAT4-A) (ST3Gal I)		
	(SIATFL)		
	beta-galactoside alpha-2,3-sialyltransferase (EC 2.4.99.4) - human		
	beta-galactoside alpha-2,3-sialyltransferase		
	Sialyltransferase 4A		
	sialyltransferase		
NP_058669.1	alpha-2,3-sialyltransferase		
	CMP-NeuAc:(beta)-N-acetylglactosaminide (alpha)2,6-sialyltransferase		
	member VI		
	CMP-NeuAc:(beta)-N-acetylglactosaminide (alpha)2,6-sialyltransferase		
	member VI		
	CMP-NeuAc:(beta)-N-acetylglactosaminide (alpha)2,6-sialyltransferase		
	member VI		
	CMP-NeuAc:(beta)-N-acetylglactosaminide (alpha)2,6-sialyltransferase		
	member VI		
	N-acetylglactosaminide alpha2,6-sialyltransferase		
NP_058669.1	alpha 2,6-sialyltransferase		
	VI		
	unnamed protein product		

NP_112227.1	sialyltransferase 7E; alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase E; GD1 alpha synthase; GalNAc alpha-2,6-sialyltransferase V; alpha-N-acetyl/galactosaminide alpha-2,6-sialyltransferase V	278 1e-074
Q9BVH7	Alpha-N-acetyl/galactosaminide alpha-2,6-sialyltransferase V (GD1 alpha synthase) (GalNAc alpha-2,6-sialyltransferase V)	278 1e-074
AAH01201.1	(ST6GalNAc V) (Sialyltransferase 7E)	278 1e-074
BAB71127.1	Sialyltransferase 7E	278 1e-074
CAD45372.1	unnamed protein product	278 1e-074
	alpha 2,6-sialyltransferase	278 1e-074
	Sialyltransferase 7	
AAH59363.1	((alpha-N-acetylneuraminyl-2,3-beta-galactosyl)-1, 3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) C	218 2e-056
	sialyltransferase 7	
	((alpha-N-acetylneuraminyl-2,3-beta-galactosyl)-1, 3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) C; alpha-N-acetyl/galactosaminide	
NP_694541.1	alpha-2,6-sialyltransferase III; sialyltransferase 7C; ST6GALNAC III	217 2e-056
BAC03611.1	unnamed protein product	217 2e-056
CAD45371.1	alpha 2,6-sialyltransferase	217 3e-056
CAC07404.1	alpha2,6-sialyltransferase	210 4e-054
BAA91281.1	unnamed protein product	209 7e-054

	sialyltransferase 7D isoform a;				
	NeuAc-alpha-2,3-Gal-beta-1,3-GalnAc-alpha-2,				
	6-sialyltransferase alpha2,6-sialyltransferase;				
	sialyltransferase 3C;				
	NeuAc-alpha-2,3-Gal-beta-1,3-GalnAc-alpha-2,				
	6-sialyltransferase IV				
NP_055218.3	sialyltransferase 7D isoform a;				208 1e-053
	NeuAc-alpha-2,3-Gal-beta-1,3-GalnAc-alpha-2,				
	6-sialyltransferase alpha2,6-sialyltransferase;				
	sialyltransferase 3C;				
	NeuAc-alpha-2,3-Gal-beta-1,3-GalnAc-alpha-2,				
	6-sialyltransferase IV				
NP_778204.1	Alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,				208 1e-053
	3-N-acetyl-galactosaminide alpha-2,6-sialyltransferase				
	(NeuAc-alpha-2,3-Gal-beta-1,3-GalnAc-alpha-2,				
	6-sialyltransferase) (ST6GalNac IV) (Sialyltransferase				
	7D) (Sialyltransferase 3C)				
Q9H4F1	N-acetylgalactosaminide alpha2,6-sialyltransferase				208 1e-053
BAA87034.1	SIAT7D protein				208 1e-053
AAH36705.1	Ski-interacting protein; nuclear receptor coactivator, 62-kD; BX42,				208 1e-053
Mm.22809	Drosophila, homolog of				587 e-167
F:2.36	Nuclear protein SkiP (Ski-interacting protein) (SNW1 protein)				
NP_036377.1	(Nuclear receptor coactivator NCoA-62)				587 e-167
Q13573	nuclear protein Skip				587 e-167
AAC15912.1	nuclear receptor coactivator NCoA-62				587 e-167
AAC31697.1	nuclear receptor coactivator NCoA-62				587 e-167
AAF23325.1	nuclear receptor coactivator NCoA-62				587 e-167
AAH40112.1	SNW1 protein				587 e-167

AAH46105.2	SNW1 protein similar to Nuclear protein SkIP (Ski-interacting protein) (SNW1	587	e-167
XP_291504.2	protein) (Nuclear receptor coactivator NCoA-62)	503	e-142
AAF01479.1	nuclear receptor coactivator NCoA-62	494	e-139
AAB48857.1	unknown	453	e-127
	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1; protease inhibitor 2 (anti-elastase), monocyte/neutrophil; protease inhibitor 2 (anti-elastase), monocyte/neutrophil derived	345	e-138
AK018226	NP_109591.1		
	Mm.92685 F:2.35		
	ILEU_HUMAN Leukocyte elastase inhibitor (LEI) (Monocyte/neutrophil elastase inhibitor) (M/NEI) (EI)	345	e-138
P30740	elastase inhibitor	345	e-138
S27383	monocyte/neutrophil elastase inhibitor	345	e-138
AAC31394.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1	345	e-138
AAH09015.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9; protease inhibitor 9 (ovalbumin type)	200	79
NP_004146.1	SPB9_HUMAN Cytoplasmic antiprotease 3 (CAP3) (CAP-3) (Protease inhibitor 9)	200	79
P50453	(Serpine B9)	200	79
B59273	protease inhibitor 9	200	79
AAC41940.1	cytoplasmic antiprotease 3	200	79
AAC50793.1	serine proteinase inhibitor	200	79
AAH02538.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9	200	79
BAB91078.1	serine protease inhibitor 9	200	79

	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8; protease inhibitor 8 (ovalbumin type)	207	2.00e-76
NP_002631.1	SPB8_HUMAN Cytoplasmic antiproteinase 2 (CAP2) (CAP-2) (Protease inhibitor 8) (Serpine B8)	207	2.00e-76
P50452	proteinase inhibitor 8	207	2.00e-76
A59273	cytoplasmic antiproteinase 2	207	2.00e-76
AAC41939.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 10; protease inhibitor 10 (ovalbumin type, bomapin)	179	4.00e-75
NP_005015.1	SB10_HUMAN Bomapin (Protease inhibitor 10) (Serpine B10)	179	4.00e-75
P48595	bomapin	179	4.00e-75
I39184	bomapin	179	4.00e-75
AAC50282.1	PTI6_HUMAN Placental thrombin inhibitor (Cytoplasmic antiproteinase) (CAP) (Protease inhibitor 6) (PI-6)	192	4.00e-75
P35237	cytoplasmic antiproteinase; CAP	192	4.00e-75
AAB30320.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6	192	4.00e-75
AAH01394.1	A Chain A, Human Plasminogen Activator Inhibitor-2. Loop (66-98) Deletion Mutant	199	5.00e-75
1BY7	A Chain A, Human Plasminogen Activator Inhibitor-2. [loop (66-98) Deletion mutant]	199	5.00e-75
1JRR	Complexed With Peptide Mimicking The Reactive Center Loop	199	3.00e-75
NP_004559.3	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6; protease inhibitor 6 (placental thrombin inhibitor)	190	74

A48681	placental thrombin inhibitor	190	3.00e-74
CAA80373.1	thrombin inhibitor	190	3.00e-74
XP_209106.1	similar to Squamous cell carcinoma antigen 2 (SCCA-2) (Leupin) serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4; protease	189	1.00e-72
NP_002965.1	inhibitor (leucine-serpin); squamous cell carcinoma antigen 2; leupin	189	1.00e-72
P48594	SCC2_HUMAN Squamous cell carcinoma antigen 2 (SCCA-2) (Leupin)	189	1.00e-72
CAA61420.1	leupin	189	1.00e-72
AAA97553.1	squamous cell carcinoma antigen 2	189	1.00e-72
AAA92602.1	squamous cell carcinoma antigen	189	1.00e-72
BAB21525.1	squamous cell carcinoma antigen 2	189	1.00e-72
AAH17401.1	Unknown (protein for MGC:27150)	189	1.00e-72
I38202	leupin precursor	189	2.00e-72
AAA36413.1	plasminogen activator inhibitor	186	2.00e-72
AAA60006.1	plasminogen activator inhibitor type 2 precursor	186	2.00e-72
NM_021301	Mm.28180	1128	0
NP_067276	F-2.35 NP_066568.2 solute carrier family 15 (H+/peptide transporter), member 2		

AAH44572.1		solute carrier family 15 (H ⁺ /peptide transporter), member 2	1128	0
		Oligopeptide transporter, kidney isoform (Peptide transporter 2)		
		(Kidney H ⁺ /peptide cotransporter) (Solute carrier family 15, member 2)		
Q16348		PEPT 2 - human	1122	0
I52481		PEPT 2	1122	0
AAB34388.1		H/peptide cotransporter	1122	0
2113198A		Caco-2 oligopeptide transporter	1122	0
AAC15477.1		solute carrier family 15 (oligopeptide transporter), member 1; peptide transporter HPEPT1	561	e-159
NP_005064.1		Oligopeptide transporter, small intestine isoform (Peptide transporter 1) (Intestinal H ⁺ /peptide cotransporter)	561	e-159
P46059		(Solute carrier family 15, member 1)	561	e-159
A56163		peptide transport protein hPEPT1 - human	561	e-159
AAA63797.1		peptide transporter	561	e-159
AAB61693.1		intestinal H ⁺ /peptide cotransporter	561	e-159
		bA551M18.1.1 (solute carrier family 15 (oligopeptide transporter) member 1)	502	e-141
CAC27442.1		pH-sensing regulatory factor - human	231	6e-060
JC5638		pH-sensing regulatory factor of peptide transporter	231	6e-060
BAA22632.1		heat shock transcription factor 1 [Homo sapiens]		
		sp Q00613 HSF1_HUMAN Heat shock factor protein 1 (HSF 1) (Heat shock transcription factor		
		1) (HSTF 1)	837	0
		heat shock transcription factor 1 - human	837	0
		heat shock factor 1	837	0
		Heat shock transcription factor 1	837	0
		heat shock transcription factor 1	837	0
		heat shock factor	835	0
X61753	Mm.18401			
A40583	9	F-2.35 NP_005517.1		
		A41137		
		AAA52695.1		
		AAH14638.1		
		AAP36015.1		
		2102256A		

NP_004497.1	heat shock transcription factor 2	261	2e-069
	Heat shock factor protein 2 (HSF 2) (Heat shock transcription factor 2) (HSTF 2)		
Q03933	heat shock transcription factor HSF2 - human	261	2e-069
A41138	HSF2	261	2e-069
AAA36017.1	Heat shock factor protein 4 (HSF 4) (Heat shock transcription factor 4) (HSTF 4) (hHSF4)		
Q9ULV5	transcription factor HSF4b isoform	253	6e-067
BAA84582.1	transcription factor HSF4	253	6e-067
BAA84581.1	heat shock transcription factor 4	246	1e-064
NP_001529.1	heat shock transcription factor 4	246	1e-064
BAA13433.1	heat shock transcription factor 4	246	1e-064
AAH05329.1	HSF2 protein	245	2e-064
AAH64622.1	Unknown (protein for MGC:75048)	245	2e-064
AAG23698.1	heat shock transcription factor 1	235	2e-061
CAB16203.1	dJ425C14.1 (heat shock transcription factor 2, variant 1)	226	8e-059
NM_013597	Mm.25068		
Q60929	1	753	0
F:2.34	myocyte-specific enhancer factor 2A, C9 form		
CAA76175.1	serum response factor-related protein	748	0
1804266B	serum response factor-related protein C9	712	0
C39481	serum response factor-related protein 9 - human (fragment)	706	0
	MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A)		
NP_005578.1	Myocyte-specific enhancer factor 2A (Serum response factor-like protein 1)	688	0
Q02078	myocyte-specific enhancer factor mef2 - human	688	0
S25831	myocyte-specific enhancer factor 2 (MEF2)	688	0
CAA48517.1	myocyte-specific enhancer factor 2A, C4 form	688	0
AAB17196.1	serum response factor-related protein	682	0
CAA44979.1	MEF2A protein	682	0
AAH13437.1			

U33557	B39481		serum response factor-related protein 4 - human	655	0
2206297A	1804266A		serum response factor-related protein C4	652	0
			Folypolyglutamate synthase, mitochondrial precursor		
	Q05932		(Folypoly-gamma-glutamate synthetase) (FPGS)	966	0
	AAH64393.1		FPGS protein	966	0
	A46281		tetrahydrofolypolyglutamate synthase (EC 6.3.2.17) - human	920	0
	AAA35852.1		folypolyglutamate synthetase	920	0
	AAA87568.1		folypolyglutamate synthetase	818	0
	AAC13871.1		folypolyglutamate synthetase	587	e-167
	NP_004948.2		folypolyglutamate synthetase; folypolyglutamate synthetase	206	2e-052
	AAP35285.1		folypolyglutamate synthase	206	2e-052
AK005342					
BAB23964.1	NP_620153.1		hypothetical protein BC018453	421	e-118
NM_016919	AAH18453.1		Similar to RIKEN cDNA 1500032H18 gene	421	e-118
NP_058615.1	NP_056534.1		collagen, type V, alpha 3 preproprotein; pro-(alpha)3(V) collagen	535	e-151
	AAF59902.1		AF177941_1 collagen type V alpha 3 chain.	535	e-151
				7.00e-	
	P12107		CA1B_HUMAN Collagen alpha 1(XI) chain precursor	258	68
				7.00e-	
	CGHU1E		collagen alpha 1(XI) chain precursor	258	68
				7.00e-	
	AAA51891.1		alpha-1 (type XI) collagen precursor	258	68
	AAF04725.1		collagen type XI alpha-1 isoform A	2.00e-	
				257	67
				2.00e-	
	NP_001845.2		alpha 1 type XI collagen Isoform A preproprotein; collagen XI, alpha-1 polypeptide	257	67
				2.00e-	
	P20908		CA15_HUMAN Collagen alpha 1(V) chain precursor	257	67

D85612	Mm.27600	BAA14323.1	collagen alpha 1(V) chain precursor	257	2.00e-67
P97305	0	CGHU1V	collagen alpha 1(V) chain precursor	257	2.00e-67
		AAA59993.1	pro-alpha-1 type V collagen	257	2.00e-67
		NP_000084.2	alpha 1 type V collagen preproprotein	257	2.00e-67
		AAF04726.1	collagen type XI alpha-a isoform B	257	2.00e-67
		NP_542196.1	alpha 1 type XI collagen isoform B preproprotein; collagen XI, alpha-1 polypeptide cytoplasmic nuclear factor of activated T-cells 3 isoform 1; nuclear factor of activated T-cells, cytoplasmic 3; T cell	257	2.00e-67
		NP_775188.1	transcription factor NFAT4	1643	0
		Q12968	Nuclear factor of activated T-cells, cytoplasmic 3 (T cell	1643	0
		A57377	transcription factor NFAT4) (NF-ATc3) (NF-AT4) (NFATx)	1643	0
		AAA86308.1	transcription factor NFATx - human	1643	0
		AAH01050.1	NFATx	1643	0
			Cytoplasmic nuclear factor of activated T-cells 3, isoform 1	1643	0
			cytoplasmic nuclear factor of activated T-cells 3 isoform 3; nuclear factor of activated T-cells, cytoplasmic 3; T cell		
		NP_775186.1	transcription factor NFAT4	1598	0
			cytoplasmic nuclear factor of activated T-cells 3 isoform 2; nuclear factor of activated T-cells, cytoplasmic 3; T cell		
		NP_004546.1	transcription factor NFAT4	1598	0
		AAA79174.1	alternative splicing form	1598	0

				cytoplasmic nuclear factor of activated T-cells 3 isoform 4; nuclear factor of activated T-cells, cytoplasmic 3; T cell	
				transcription factor NFAT4	1598 0
				transcription factor NFATx4	1591 0
				transcription factor NFATx3	1591 0
				transcription factor NFATx2	1591 0
				Nuclear factor of activated T-cells, cytoplasmic 4 (T cell	
				transcription factor NFAT3) (NF-ATc4) (NF-AT3)	495 e-139
				NF-AT3 gene product	495 e-139
				cytoplasmic nuclear factor of activated T-cells 4; nuclear factor of	
				activated T-cells, cytoplasmic 4; T cell transcription	
				factor NFAT3	494 e-139
				Cytoplasmic nuclear factor of activated T-cells 4	494 e-139
				NFATC4 protein	491 e-138
NM_008047					
NP_032073.1	Mm.22763	F:2.31		follostatin-like 1 precursor; follistatin-related protein	572 e-162
				FSL1_HUMAN Follistatin-related protein 1 precursor (Follistatin-like 1)	572 e-162
				follistatin-related protein	572 e-162
				follistatin-related protein precursor	572 e-162
				follistatin-related protein (FRP)	572 e-162
				follistatin-like 1	572 e-162
					6.00e-
AF060517	Mm.17415			follistatin-related protein	244 64
O88874	5	F:2.31		CYCK_HUMAN Cyclin K	456 e-128
				AAD09978.	
				1	
				cyclin K	456 e-128
				cyclin K	456 e-128

NM_013699	I49257	Mm.28052	F:2.31	NP_003849.2	cyclin K		456	e-128
				AAH15935.1	cyclin K		456	e-128
				AAH15935.1	cyclin K		456	e-128
				AAP35596.1	cyclin K		456	e-128
NM_013699	I49257	Mm.28052	F:2.31	LBP-1a=transcription factor binding to initiation site of HIV-1 {alternatively spliced} [human, Namalwa cells, Peptide, 504 aa]			940	0
				AAB29975.1	transcription factor LBP1a - human		937	0
				A56205	unnamed protein product		932	0
				BAB14501.1	LBP-1b=transcription factor binding to initiation site of HIV-1 {alternatively spliced} [human, Namalwa cells, Peptide, 541 aa]		922	0
				AAB29977.1	transcription factor LBP-1b		921	0
				AAF32274.1	upstream binding protein 1 (LBP-1a)		919	0
				NP_055332.2	upstream binding protein 1 (LBP-1a)		919	0
				AAH47235.1	transcription factor LBP1b - human		914	0
				B56205	transcription factor CP2; Transcription factor CP2, alpha globin		731	0
				NP_005644.2	transcription factor LBP1c - human		731	0
NM_013699	NP_035768.1	Mm.28683	F:2.31	C56205	LBP-1c=transcription factor alpha-globin CP2 homolog {alternatively spliced} [human, Namalwa cells, Peptide, 502 aa]		731	0
				AAB29976.1	Transcription factor CP2		731	0
				AAH03634.1	transcription factor LSF		729	0
				AAA21324.1	alpha-globin transcription factor CP2 - human		721	0
				A42030	Transferrin receptor protein 1 (TfR1) (TR) (TfR) (Tfrr) (CD71 antigen) (T9) (p90)		1196	0
				P02786	transferrin receptor - human		1196	0
				JXHU	transferrin receptor		1196	0
				AAA61153.1	transferrin receptor		1196	0
				1011297A	transferrin receptor		1196	0
				AAF04564.1	transferrin receptor		1195	0

AAH01188.1	TfRC protein	1195	0
	Chain C, Hemochromatosis Protein Hfe Complexed With Transferrin Receptor		
1DE4 C		1023	0
	Chain F, Hemochromatosis Protein Hfe Complexed With Transferrin Receptor		
1DE4 F		1023	0
	Chain I, Hemochromatosis Protein Hfe Complexed With Transferrin Receptor		
1DE4 I		1023	0
	Chain A, Crystal Structure Of The Ectodomain Of Human Transferrin Receptor		
1CX8 A		1020	0
	Chain B, Crystal Structure Of The Ectodomain Of Human Transferrin Receptor		
1CX8 B		1020	0
	Chain C, Crystal Structure Of The Ectodomain Of Human Transferrin Receptor		
1CX8 C		1020	0
	Chain D, Crystal Structure Of The Ectodomain Of Human Transferrin Receptor		
1CX8 D		1020	0
	Chain E Crystal Structure Of The Ectodomain Of Human Transferrin Receptor		
1CX8 E		1020	0
	Chain F, Crystal Structure Of The Ectodomain Of Human Transferrin Receptor		
1CX8 F		1020	0
	Chain G Crystal Structure Of The Ectodomain Of Human Transferrin Receptor		
1CX8 G		1020	0
	Chain H, Crystal Structure Of The Ectodomain Of Human Transferrin Receptor		
1CX8 H		1020	0
NP_003218.2	transferrin receptor 2	545 e-154	
Q9UP52	Transferrin receptor protein 2 (TfR2)	545 e-154	
AAD45561.1	transferrin receptor 2 alpha	545 e-154	
AAC78796.1	transferrin-receptor2	498 e-140	
BAA91153.1	unnamed protein product	315 5e-085	

AAC83972.1	prostate-specific membrane antigen	228 6e-059
	folate hydrolase (prostate-specific membrane antigen) 1; folate hydrolase 1 (prostate-specific membrane antigen);	
NP_004467.1	glutamate carboxylase II	228 6e-059
	Glutamate carboxypeptidase II (Membrane glutamate carboxypeptidase) (mGCP) (N-acetylated-alpha-linked acidic dipeptidase I) (NAALADase I) (Pteroyl/poly-gamma-glutamate carboxypeptidase) (Folypoly-gamma-glutamate carboxypeptidase) (FGCP) (Folate hydrolase 1) (Prostate-specific membrane antigen) (PSMA) (PSM)	
Q04609	prostate-specific membrane antigen - human	228 6e-059
A56881	prostate-specific membrane antigen	228 6e-059
AAA60209.1	folypoly-gamma-glutamate carboxypeptidase	228 6e-059
AAD51121.1	prostate-specific membrane antigen	228 6e-059
AAM34479.1	N-acetylated alpha-linked acidic dipeptidase 2; N-acetylated alpha-linked acidic dipeptidase II	228 6e-059
NP_005458.1	N-acetylated-alpha-linked acidic dipeptidase II (NAALADase II)	216 3e-055
Q9Y3Q0	NAALADase II protein	216 3e-055
CAB39967.1	myogenin; Myogenic factor-4; myogenin; myogenic factor 4	216 3e-055
NM_031189	MYOG_HUMAN Myogenin (Myogenic factor Myf-4)	
NP_002470.2	myogenin	412 e-115
P15173	Myf4 protein	412 e-115
A41128	AF050501_1 myogenin	412 e-115
CAA44080.1	Myf-4 protein (AA 1-246)	409 e-114
AAG22573.1	Myf-4 protein (AA 1-246)	389 e-108
CAA35641.1	Myf-4 protein (AA 1-246)	2.00e-75
AB035725	Myf-4 protein (AA 1-246)	281 75
NP_062640	NSAP1 protein	852 0

synaptotagmin binding, cytoplasmic RNA interacting protein;			
NP_006363.3	NS1-associated protein 1	852	0
AAC12926.1	Gry-rbp	852	0
AAK59703.1	hnRNP Q3	852	0
AAK59705.1	hnRNP Q1	852	0
AAH15575.1	SYNCRIP protein	832	0
AAH32643.1	SYNCRIP protein	763	0
AAK59704.1	hnRNP Q2	761	0
NP_005817.1	heterogeneous nuclear ribonucleoprotein R	722	0
O43390	Heterogeneous nuclear ribonucleoprotein R (hnRNP R)	722	0
T02673	heterogeneous nuclear ribonucleoprotein R - human	722	0
AAC39540.1	heterogeneous nuclear ribonucleoprotein R	722	0
AAH01449.1	HNRPR protein	717	0
CAE45953.1	hypothetical protein	665	0
XP_001541.2	heterogeneous nuclear ribonucleoprotein R	606	e-173
NM_008885		6.00e-	
NP_032911.1	Mm.1237	246	65
NP_000295.1	peripheral myelin protein 22; growth arrest-specific 3	246	65
NP_696996.1	peripheral myelin protein 22; growth arrest-specific 3	246	65
NP_696997.1	peripheral myelin protein 22; growth arrest-specific 3	246	65
Q01453	PM22_HUMAN Peripheral myelin protein 22 (PMP-22)	246	65
JN0503	peripheral myelin protein 22	246	65
AAA58495.1	peripheral myelin protein 22	246	65
AAA36457.1	peripheral myelin protein 22	246	65

S28184

1813206B	mitogen-activated protein kinase	639	0
CAA77752.1	41kD protein kinase	638	0
1813206A	mitogen-activated protein kinase	638	0
	mitogen-activated protein kinase 1; extracellular signal-regulated kinase 2; protein tyrosine kinase ERK2; mitogen-activated protein kinase 2	637	0
NP_002736.2	Structure Of Penta Mutant Human Erk2 Map Kinase Complexed With A Specific Inhibitor Of Human P38 Map Kinase	625	e-179
1PME	bromodomain containing protein 2; female sterile homeotic-related gene 1	1083	0
NM_010238		1083	0
NP_034368	Bromodomain-containing protein 2 (RING3 protein) (O27.1.1)	1083	0
	BAA07641.1 KIAA9001	1083	0
	CAA43996.1 FSH	1083	0
	O14.1.1 (bromodomain-containing protein 2 (RING3, KIAA9001), isoform 1)	1082	0
	O27.1.1 (bromodomain-containing protein 2 (RING3, KIAA9001), isoform 1)	1082	0
CAC69989.1	BRD2 protein	1066	0
AAH63840.1	female sterile homeotic (fsh) homolog RING3 - human	1048	0
A56619	putative	1048	0
AAA68890.1	kinase	1046	0
CAA65450.1	KIAA0043	642	0
BAA05393.2	bromodomain containing protein 3; RING3-like gene;		
NP_031397.1	bromodomain-containing 3; open reading frame X	642	0
Q15059	BRD3_HUMAN Bromodomain-containing protein 3	642	0
AAO22237.1	BRD4-NUT fusion oncoprotein	577	e-164
AAC27978.1	R31546_1	577	e-164
	bromodomain-containing protein 4 isoform short; chromosome-associated protein	577	e-164
NP_055114.1			

NM_016860	Mm.13276			ARP1 actin-related protein 1 homolog A, centractin alpha; ARP1 (actin-related protein 1, yeast) homolog A (centractin alpha); centractin alpha; actin-RPV; centrosome-associated actin homolog; ARP1, yeast homolog	755	0
P42024	4	F:2.27	NP_005727.1	A Alpha-centractin (Centractin) (Centrosome-associated actin homolog)	755	0
	P42024			(Actin-RPV) (ARP1)	755	0
	S29089			alpha-centractin - human	755	0
	CAA78701.1			actin-related protein	755	0
	AAB23391.1			actin-related protein, actin-RPV=dynactin complex major component [human, N-Tera teratocarcinoma, Peptide, 376 aa]	755	0
	CAA57690.1			alpha-centractin	755	0
	CAC08404.1			bA18114.9 (novel protein similar to beta-centractin (ACRTR1B))	755	0
	AAH00693.1			ARP1 actin-related protein 1 homolog A, centractin alpha	755	0
	AAH26016.1			ACTR1A protein	755	0
	1818358A			actin-related protein	753	0
				ARP1 actin-related protein 1 homolog B, centractin beta; centractin beta; ARP1 (actin-related protein 1, yeast) homolog B	709	0
	NP_005726.1			(centractin beta); PC3; ARP1, yeast homolog B	709	0
	P42025			Beta-centractin (Actin-related protein 1B) (ARP1B)	709	0
	CAA57691.1			beta-centracetin	709	0
	AAH04374.1			ARP1 actin-related protein 1 homolog B, centractin beta	709	0
	AAH10090.1			ARP1 actin-related protein 1 homolog B, centractin beta	709	0
	AAH10090.1			ARP1 actin-related protein 1 homolog B, centractin beta	708	0
	CAA57692.1			beta-centractin	616	e-176
				actin, gamma 1 propeptide; cytoskeletal gamma-actin; actin, cytoplasmic 2	425	e-118
	NP_001605.1			Actin, cytoplasmic 2 (Gamma-actin)	425	e-118
	P02571			actin gamma 1 - human	425	e-118
	ATHUG				425	e-118

CAA27723.1	gamma-actin	425	e-118
AAA51579.1	gamma-actin	425	e-118
AAH00292.1	Actin, gamma 1	425	e-118
AAH01920.1	ACTG1 protein	425	e-118
AAH07442.1	Actin, gamma 1	425	e-118
AAH09848.1	Actin, gamma 1	425	e-118
AAH10999.1	ACTG1 protein	425	e-118
AAH12050.1	Actin, gamma 1	425	e-118
AAH15005.1	ACTG1 protein	425	e-118
AAH15695.1	Actin, gamma 1	425	e-118
AAH15779.1	ACTG1 protein	425	e-118
AAH18774.1	ACTG1 protein	425	e-118
AAH53572.1	Actin, gamma 1	425	e-118
NP_005150.1	actin, alpha, cardiac muscle precursor	425	e-118
P04270	Actin, alpha cardiac	425	e-118
ATHUC	actin, cardiac muscle - human	425	e-118
AAB59619.1	alpha-cardiac actin	425	e-118
AAH09978.1	Actin, alpha, cardiac muscle precursor	425	e-118
JC5818	gamma-actin - human	425	e-118
NP_001092.1	beta actin; beta cytoskeletal actin	424	e-118
P02570	Actin, cytoplasmic 1 (Beta-actin)	424	e-118
ATHUB	actin beta - human	424	e-118
CAA25099.1	unnamed protein product	424	e-118
AAA51567.1	cytoplasmic beta actin	424	e-118
AAH01301.1	Beta actin	424	e-118
AAH02409.1	Beta actin	424	e-118
AAH04251.1	Beta actin	424	e-118
AAH13380.1	Beta actin	424	e-118
AAH14861.1	Beta actin	424	e-118
AAP22343.1	unknown	424	e-118

NM_009928		424	e-118
NP_034058.1	Mm.4352 F:2.26	AAH08633.1	actin, beta
		AAC78500.1	type XV collagen
		NP_001846.2	alpha 1 type XV collagen precursor; collagen XV, alpha-1 polypeptide
		P39059	CA1E_HUMAN Collagen alpha 1(XV) chain precursor
		A53317	collagen alpha 1(XV) chain precursor
		AAA58429.1	alpha-1 type XV collagen
		BAA04762.1	alpha 1(XV) collagen chain
		NP_569711.1	alpha 1 type XVIII collagen isoform 3 precursor; endostatin
		AAH33715.1	Similar to collagen, type XVIII, alpha 1
		NP_569712.1	alpha 1 type XVIII collagen isoform 2 precursor; endostatin
		AAC39659.1	type XVIII collagen
		NP_085059.1	alpha 1 type XVIII collagen isoform 1 precursor; endostatin
		P39060	CA1H_HUMAN Collagen alpha 1(XVIII) chain precursor [Contains: Endostatin]
		AAC39658.1	type XVIII collagen
		CAB90482.1	human type XVIII collagen
		A53019	collagen alpha 1(XVIII) chain
		AAA51864.1	collagen type XVIII alpha 1

NM_016762	NP_058042.1	Mm.3511	F:2.26	CAD38787.1	hypothetical protein	1746	0
				NP_002371.2	matrilin 2 precursor	1746	0
				O00339	MTN2_HUMAN Matrilin-2 precursor	1744	0
				AAC51260.2	matrilin-2 precursor	1744	0
				AAH10444.1	matrilin 2	1703	0
				NP_085072.1	matrilin 2 precursor	1703	0
				T46488	hypothetical protein DKFZp434J065.1	1341	0
				CAB70853.1	hypothetical protein	1341	0
				BAB55358.1	unnamed protein product	993	0
				BAC11648.1	unnamed protein product	794	0
				O95460	MTN4_HUMAN Matrilin-4 precursor	382 e-105	
				CAC18105.1	dJ453C12.1.2 (matrilin 4)	382 e-105	
				NP_002372.1	matrilin 3 precursor	2.00e-	
				O15232	MTN3_HUMAN Matrilin-3 precursor	359	98
				CAA12110.1	matrilin-3	2.00e-	
					potassium inwardly-rectifying channel J12; ATP-sensitive inward rectifier potassium channel 12; potassium	359	98
NM_010603	A54714	Mm.4970	F:2.26	NP_066292.2	inwardly-rectifying channel, subfamily J, inhibitor 1	794	0
				BAC02718.1	inward rectifier potassium channel Kir2.2	794	0
				AAH27982.1	Potassium inwardly-rectifying channel J12	794	0
					ATP-sensitive inward rectifier potassium channel 12 (Potassium channel, inwardly rectifying, subfamily J, member 12)		
				Q14500	(Inward rectifier K+ channel Kir2.2) (IRK2)	787	0
				I52864	potassium channel alpha subunit - human	787	0
				AAA65122.1	potassium channel alpha subunit	787	0

Q15756	Inward rectifying K ⁺ channel negative regulator Kir2.2v	756	0
S71341	inward rectifier potassium channel chain Kir2.2 - human	756	0
AAC50615.1	inward rectifying K ⁺ channel negative regulator Kir2.2v potassium inwardly-rectifying channel J2; inward rectifier potassium channel 2; inward rectifier K ⁺ channel KIR2.1; cardiac inward rectifier potassium channel	756	0
NP_000882.1	Inward rectifier potassium channel 2 (Potassium channel, inwardly rectifying, subfamily J, member 2) (Inward rectifier K ⁺ channel Kir2.1) (Cardiac inward rectifier potassium channel) (IRK1)	593	e-169
P48049			
I38727	cardiac inward rectifier potassium channel - human	593	e-169
AAA91781.1	inward rectifying potassium channel	593	e-169
AAC50072.1	cardiac inward rectifier potassium channel	593	e-169
AAA64282.1	inward rectifier potassium channel	593	e-169
AAB50277.1	inward rectifier K ⁺ channel protein	593	e-169
AAB88797.1	inward rectifier potassium channel	593	e-169
AAF73241.1	inwardly-rectifying potassium channel Kir2.1	593	e-169
AAF73242.1	inwardly-rectifying potassium channel Kir2.1	593	e-169
2105159A	inward rectifier K channel	593	e-169
AAC39555.1	inwardly rectifying potassium channel Kir 2.1 potassium inwardly-rectifying channel J4; inward rectifier K ⁺ channel	590	e-168
NP_004972.1	Kir2.3; hippocampal inward rectifier potassium channel potassium inwardly-rectifying channel J4; inward rectifier K ⁺ channel	523	e-148
NP_690607.1	Kir2.3; hippocampal inward rectifier potassium channel Inward rectifier potassium channel 4 (Potassium channel, inwardly rectifying, subfamily J, member 4) (Inward rectifier K ⁺ channel Kir2.3) (Hippocampal inward rectifier) (HIR) (HRK1) (HIRK2)	523	e-148
P48050			
I38521	inwardly rectifying potassium channel, hippocampal - human	523	e-148

AAA19962.1	inwardly rectifying potassium channel; inward rectifier	523	e-148
AAA66076.1	inward rectifier K ⁺ channel protein	523	e-148
A54852	potassium rectifier protein, brain. - human	521	e-147
AAC60632.1	HRK1	521	e-147
AAC01951.1	inward rectifying K ⁺ channel negative regulator	493	e-139
	potassium inwardly-rectifying channel J14; inwardly rectifying		
NP_037480.1	potassium channel KIR2.4	454	e-127
	potassium inwardly-rectifying channel J14; inwardly rectifying		
NP_733838.1	potassium channel KIR2.4	454	e-127
AAD51376.1	inward rectifier potassium channel	454	e-127
AAF97619.1	inwardly rectifying potassium channel Kir2.4; IRK4	454	e-127
AAH35918.1	Potassium inwardly-rectifying channel J14	454	e-127
NM_007802			
NP_031828.1	Mm.3109 F:2.25	608	e-174
	cathepsin K preproprotein; cathepsin X; cathepsin O1; cathepsin O2	608	e-174
P43235	CATK_HUMAN Cathepsin K precursor (Cathepsin O) (Cathepsin O2)	608	e-174
JC2476	cathepsin K (EC 3.4.22.-) precursor	608	e-174
CAA57649.1	Cathepsin O	608	e-174
AAA65233.1	cathepsin O	608	e-174
AAB35521.1	cathepsin O2	608	e-174
AAA95998.1	cathepsin X	605	e-173
7PCK	A Chain A, Crystal Structure Of Wild Type Human Procathepsin	580	e-165
7PCK	B Chain B, Crystal Structure Of Wild Type Human Procathepsin K	580	e-165
7PCK	C Chain C, Crystal Structure Of Wild Type Human Procathepsin K	580	e-165
7PCK	D Chain D, Crystal Structure Of Wild Type Human Procathepsin K	580	e-165
1BY8	A Chain A, The Crystal Structure Of Human Procathepsin K	580	e-165
	Crystal Structure Of The Cysteine Protease Human Cathepsin K In Complex With The		
1ATK	Covalent Inhibitor E-64	402	e-112
	A Chain A, Crystal Structure Of Cathepsin K Complexed With A Potent Vinyl Sulfone		
1MEM	Inhibitor	402	e-112

1AU4	Crystal Structure Of The Cysteine Protease Human Cathepsin K In Complex With A Covalent Pyrrolidinone Inhibitor	402 e-112
1AU0	Crystal Structure Of The Cysteine Protease Human Cathepsin K In Complex With A Covalent Symmetric Diacylaminoethyl Ketone Inhibitor	402 e-112
1AU2	Crystal Structure Of The Cysteine Protease Human Cathepsin K In Complex With A Covalent Propanone Inhibitor	402 e-112
1AU3	Crystal Structure Of The Cysteine Protease Human Cathepsin K In Complex With A Covalent Pyrrolidinone Inhibitor	402 e-112
1AYU	Crystal Structure Of Cysteine Protease Human Cathepsin K In Complex With A Covalent Symmetric Biscarbohydrazide Inhibitor	402 e-112
1AYV	Crystal Structure Of Cysteine Protease Human Cathepsin K In Complex With A Covalent Thiazolhydrazide Inhibitor	402 e-112
1AYW	Crystal Structure Of Cysteine Protease Human Cathepsin K In Complex With A Covalent Benzoyloxybenzoylcarbohydrazide Inhibitor	402 e-112
1BGO	Crystal Structure Of Cysteine Protease Human Cathepsin K In Complex With A Covalent Peptidomimetic Inhibitor	402 e-112
1NL6	A Chain A, Crystal Structure Of The Cysteine Protease Human Cathepsin K In Complex With A Covalent Azepanone Inhibitor	402 e-112
1NL6	B Chain B, Crystal Structure Of The Cysteine Protease Human Cathepsin K In Complex With A Covalent Azepanone Inhibitor	402 e-112
1NLJ	A Chain A, Crystal Structure Of The Cysteine Protease Human Cathepsin K In Complex With A Covalent Azepanone Inhibitor	402 e-112
1NLJ	B Chain B, Crystal Structure Of The Cysteine Protease Human Cathepsin K In Complex With A Covalent Azepanone Inhibitor	402 e-112
AAH02642.1	cathepsin	402 e-112
NP_004070.3	cathepsin S preproprotein	362 e-100
P25774	CATS_HUMAN Cathepsin S precursor	361 e-99
		1.00e-99

Accession	Protein Name	Length	Score	Model
AAC37592.1	cathepsin S	359	99	4.00e-
A42482	cathepsin S (EC 3.4.22.27) precursor	358	99	6.00e-
AAA35655.1	cathepsin	358	99	6.00e-
AAB22005.1	cathepsin S	358	99	6.00e-
NP_001324.2	cathepsin L2 preproprotein; cathepsin U; cathepsin V	330	90	1.00e-
O60911	CSL2_HUMAN Cathepsin L2 precursor (Cathepsin V) (Cathepsin U)	330	90	1.00e-
BAA25909.1	cathepsin V	330	90	1.00e-
AAC23598.1	cathepsin U	330	90	1.00e-
BAA34365.1	cathepsin L2	330	90	1.00e-
AAH23504.1	similar to cathepsin L	330	90	1.00e-
NM_025812	Mm.15085			
NP_080088	F:2.25 6			
NP_060670.1	high-mobility group 20A	621	e-177	
BAA91782.1	unnamed protein product	621	e-177	
AAF66706.1	HMG domain protein HMGX1	621	e-177	
CAB90816.1	HMG20A	621	e-177	
AAH21959.1	High-mobility group 20A	621	e-177	
AAP35362.1	high-mobility group 20A	621	e-177	
AAG01174.1	smarce1-related protein	270	1e-071	

NM_010828	Mm.27232	AAF66707.1	HMG domain protein HMGX2	270	1e-071
NIP_034958.1	1	CAB90809.2	HMG20B	270	1e-071
		AAG60060.1	structural DNA-binding protein BRAF35	270	1e-071
		AAH02552.1	HMG20B protein	270	1e-071
		AAH03505.2	HMG20B protein	270	1e-071
		AAH04408.2	HMG20B protein	270	1e-071
		BAC03510.1	unnamed protein product	218	6e-056
		AAC62837.1	R31109_1	213	2e-054
		AAF76253.1	high-mobility group 20B	213	2e-054
		AAH21585.1	HMG20B protein	213	2e-054
NM_010828	Mm.27232	AAC51114.1	MSG1-related protein	380	e-105
NIP_034958.1	1	AAF01264.1	p35srj isoform MRG1	380	e-105
	F:2.25	NP_006070.2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	269	5e-072
			CIT2_HUMAN Cbp/p300-interacting transactivator 2 (MSG-related protein 1) (MRG1 protein) (P35srj)	269	5e-072
		Q99967		269	5e-072
		AAD10055.1	p35srj	269	5e-072
		AAF01263.1	p35srj	269	5e-072
		AAH04377.1	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	269	5e-072
NM_033620					
NIP_296369.1	Mm.72062	AAK27891.1	atypical PKC isotype-specific interacting protein long variant	2023	0.0
	F:2.25	AAL76043.1	partitioning-defective 3 protein splice variant b	2023	0.0
			partitioning-defective protein 3 homolog; atypical PKC isotype-specific Interacting protein	2018	0.0
		NP_062565.2	protein		
			PAD3_HUMAN Partitioning-defective 3 homolog (PARD-3) (PAR-3) (Atypical PKC isotype-specific interacting protein) (ASIP) (CTCL tumor antigen se2-5) (PAR3-alpha)	2018	0.0
		Q8TEW0		2018	0.0
		AAL76042.1	partitioning-defective 3 protein splice variant a	1935	0.0
		AAL76044.1	partitioning-defective 3 protein splice variant d	1925	0.0
		AAL76046.1	partitioning-defective 3 protein splice variant f		

	AAK69193.1			atypical PKC isotype-specific interacting protein long variant b	1843	0.0
	AAF71530.1			partitioning-defective 3 splice variant c	1836	0.0
	AAL76045.1			partitioning-defective 3 protein splice variant e	1784	0.0
	BAC54037.1			PAR3	1784	0.0
	AAK27892.1			atypical PKC isotype-specific interacting protein short variant	1569	0.0
	AAK69192.1			atypical PKC isotype-specific interacting protein short variant b	1471	0.0
	AAN75698.1			SE2-5L16 protein	1430	0.0
NM_010823					1027	0
NP_034953.1	NP_005364.1	F:2.24	Mm.4864	myeloproliferative leukemia virus oncogene; thrombopoietin receptor		
				TPOR_HUMAN Thrombopoietin receptor precursor (TPO-R) (Myeloproliferative		
	P40238			leukemia protein) (C-mpl) (CD110 antigen)	1027	0
	A45266			MPL-P protein precursor	1027	0
	AAA69971.1			c-myeloproliferative leukemia virus type P	1027	0
	AAB08424.1			thrombopoietin receptor	1027	0
	AAB08425.1			thrombopoietin receptor	1011	0
	CAB92756.1			dJ92O14.2 (myeloproliferative leukemia virus oncogene)	976	0
	B45266			MPL-K protein precursor	816	0
	AAA69972.1			c-myeloproliferative leukemia virus type K	816	0
				cysteine and glycine-rich protein 3; LIM domain only 4 (cardiac LIM		
				protein); cardiac LIM protein; cysteine- and		
				glycine-rich protein 3; cardiac LIM domain protein	419	e-117
NM_013808	NP_003467.1	F:2.24	Mm.17235	LIM domain protein, cardiac (Muscle LIM protein) (Cysteine-rich		
S57472				protein 3) (CRP3)	419	e-117
	P50461			LIM domain protein	419	e-117
	AAA91104.1			LIM protein MLP	419	e-117
	AAA92571.1			LIM protein MLP	419	e-117
	AAD00183.1			LIM protein MLP	419	e-117
	AAD00189.1			LIM protein MLP	419	e-117
	AAH05900.1			Cysteine and glycine-rich protein 3	419	e-117
	AAH24010.1			Cysteine and glycine-rich protein 3	419	e-117

AAH57221.1	Cysteine and glycine-rich protein 3	419	e-117
AAF28868.1	myogenic factor LIM3	417	e-116
NP_001312.1	cysteine and glycine-rich protein 2; LIM domain only 5, smooth muscle; SmLIM	289	5e-078
Q16527	CSR2_HUMAN Smooth muscle cell LIM protein (Cysteine-rich protein 2) (CRP2) (LIM-only protein 5)	289	5e-078
AAC27344.1	smooth muscle LIM protein	289	5e-078
AAC51753.1	cysteine and glycine-rich protein 2	289	5e-078
AAC51755.1	cysteine and glycine-rich protein 2	289	5e-078
AAH00992.1	cysteine and glycine-rich protein 2	289	5e-078
NP_004069.1	cysteine and glycine-rich protein 1; cysteine-rich protein; LIM-domain protein	287	1e-077
P21291	Cysteine-rich protein 1 (CRP1) (CRP)	287	1e-077
S12658	cysteine-rich protein - human	287	1e-077
AAA58431.1	cysteine-rich protein	287	1e-077
AAA35720.1	cysteine-rich protein	287	1e-077
AAA35720.1	Cysteine and glycine-rich protein 1	287	1e-077
AAH04265.1	Similar to cysteine and glycine-rich protein 1	238	1e-062
AK002523			
NP_573448	Mm.27792 F:2.24 leucine zipper domain protein	444	e-124
NP_078865.1	leucine zipper domain protein	444	e-124
BAB15331.1	unnamed protein product	444	e-124
CAB66610.1	hypothetical protein	444	e-124
AAH12901.1	Leucine zipper domain protein	444	e-124
NM_009395			
NP_033421.2	Mm.10331 F:2.24 tumor necrosis factor-alpha-induced protein B12 - human	679	0
NP_066960.1	tumor necrosis factor, alpha-induced protein 1	625	e-178
Q13829	Tumor necrosis factor, alpha-induced protein 1, endothelial (B12 protein)	625	e-178
AAA58385.1	B12 protein	625	e-178

AAH01643.1	Tumor necrosis factor, alpha-induced protein 1	625	e-178
AAH01949.1	TNFAIP1 protein	625	e-178
AAL38649.1	tumor necrosis factor, alpha-induced protein 1 (endothelial) potassium channel tetramerisation domain containing 10; MSTP028	625	e-178
NP_114160.1	protein	439	e-122
AAG39279.1	MSTP028	439	e-122
AAH40062.1	Potassium channel tetramerisation domain containing 10	439	e-122
BAB55188.1	unnamed protein product potassium channel tetramerisation domain containing 13; polymerase	437	e-122
NP_849194.1	delta-interacting protein 1; TNFAIP1-like	419	e-116
AAL55757.1	unknown	419	e-116
AAH36228.1	Potassium channel tetramerisation domain containing 13	419	e-116
AAK27301.1	TNFAIP1-like protein	418	e-116
AAL14962.1	polymerase delta-interacting protein 1	409	e-113
NM_010137	endothelial PAS domain protein 1	1394	0
P97481	Endothelial PAS domain protein 1 (EPAS-1) (Member of PAS protein 2) (MOP2) (Hypoxia-inducible factor 2 alpha) (HIF-2 alpha)		
Q99814	(HIF2 alpha) (HIF-1 alpha-like factor) (HLF)	1394	0
AAH51338.1	Endothelial PAS domain protein 1	1394	0
AAB41495.1	endothelial PAS domain protein 1	1392	0
AAC51212.1	PAS protein 2 hypoxia-inducible factor 1, alpha subunit isoform 2; ARNT interacting	1379	0
NP_851397.1	protein; member of PAS superfamily 1	551	e-156
BAB70608.1	hypoxia-inducible factor 1 alpha variant hypoxia-inducible factor 1, alpha subunit isoform 1; ARNT interacting	551	e-156
NP_001521.1	protein; member of PAS superfamily 1 Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha) (ARNT	551	e-156
Q16665	interacting protein) (Member of PAS protein 1) (MOP1)	551	e-156

I38972	hypoxia-inducible factor 1 alpha - human	551	e-156
AAC50152.1	hypoxia-inducible factor 1 alpha	551	e-156
AAC51210.1	ARNT interacting protein	551	e-156
AAF20139.1	hypoxia-inducible factor 1 alpha	551	e-156
AAF20140.1	hypoxia-inducible factor 1 alpha	551	e-156
AAF20149.1	hypoxia-inducible factor 1 alpha	551	e-156
AAG43026.1	hypoxia-inducible factor 1 alpha subunit	551	e-156
AAH12527.1	Hypoxia-inducible factor 1, alpha subunit, isoform 1	551	e-156
	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)		
AAP88778.1		551	e-156
2114407A	hypoxia-inducible factor 1	551	e-156
AAC68568.1	hypoxia-inducible factor 1 alpha subunit	549	e-155
	hypoxia-inducible factor-3 alpha isoform c; inhibitory PAS domain protein		
NP_690008.1		363	e-100
AAL69947.1	inhibitory PAS domain protein	363	e-100
	hypoxia-inducible factor-3 alpha isoform a; inhibitory PAS domain protein		
NP_690007.1		363	e-100
JC7771	hypoxia Inducible factor-3 alpha - human	363	e-100
AAD22668.1	Putative homolog of hypoxia inducible factor three alpha	363	e-100
BAB69689.1	hypoxia-inducible factor-3 alpha	363	e-100
BAB55324.1	unnamed protein product	363	1e-099
	hypoxia-inducible factor-3 alpha isoform b; inhibitory PAS domain protein		
NP_071907.2		328	4e-089
AF378762	tumor endothelial marker 8 isoform 1 precursor; anthrax toxin receptor; tumor		
NP_115584.1	endothelial marker 8, isoform 3 precursor	881	0
Q9H6X2	ATR_HUMAN Anthrax toxin receptor precursor (Tumor endothelial marker 8)	881	0
AAK52094.1	tumor endothelial marker 8 precursor	881	0
	tumor endothelial marker 8 isoform 2 precursor; anthrax toxin receptor; tumor		
NP_444262.1	endothelial marker 8, isoform 3 precursor	600	e-171

AAI26496.1	AF421380_1 anthrax toxin receptor	600 e-171
	tumor endothelial marker 8 isoform 3 precursor; anthrax toxin receptor; tumor	
NP_060623.2	endothelial marker 8, isoform 3 precursor	563 e-159
AAH12074.1	Similar to tumor endothelial marker 8	563 e-159
BAC03731.1	unnamed protein product	486 e-136
BAA91707.1	unnamed protein product	374 e-103
		9.00e-
BAB15128.1	unnamed protein product	357 98
		2.00e-
NP_477520.1	capillary morphogenesis protein-2	223 57
		2.00e-
BAB70976.1	unnamed protein product	223 57
		3.00e-
XP_113625.3	similar to hypothetical protein 4933430J11 [Mus musculus]	216 55
		2.00e-
P58335	CMG2_HUMAN Capillary morphogenesis protein-2 precursor (CMG-2)	209 53
		2.00e-
AAK77222.1	capillary morphogenesis protein-2	209 53
		2.00e-
AAH34001.1	Similar to RIKEN cDNA 2310046B19 gene	203 51
NP_003347.1	uncoupling protein 3 isoform UCP3L; Uncoupling protein-3	531 e-151
P55916	UCP3_HUMAN Mitochondrial uncoupling protein 3 (UCP 3)	531 e-151
JC5522	uncoupling protein UCP3, mitochondrial	531 e-151
AAC51367.1	UCP3	531 e-151
AAC51369.1	uncoupling protein 3	531 e-151
AAC51767.1	uncoupling protein-3	531 e-151
AAG02284.1	AF050113_1 uncoupling protein-3	531 e-151
AAC18822.1	uncoupling protein 3	525 e-149

NM_009464

NP_033490.1 Mm.6254 F:2.23

AAC51785.1	uncoupling protein 3	510 e-145
NP_073714.1	uncoupling protein 3 isoform UCP3S; Uncoupling protein-3	464 e-131
AAC51356.1	UCP3S	464 e-131
AAB48411.1	uncoupling protein-2	457 e-129
NP_003346.2	uncoupling protein 2; Uncoupling protein-2	456 e-128
P55851	UCP2_HUMAN Mitochondrial uncoupling protein 2 (UCP 2) (UCPH)	456 e-128
AAC51336.1	UCP2	456 e-128
AAC39690.1	uncoupling protein 2	456 e-128
AAD21151.1	uncoupling protein-2	456 e-128
AAH11737.1	uncoupling protein 2 (mitochondrial, proton carrier)	456 e-128
AAB53091.1	uncoupling protein homolog	456 e-128
CAA11402.1	uncoupling protein 2	456 e-128
		6.00e-
NP_068605.1	uncoupling protein 1; mitochondrial brown fat uncoupling protein	345 95
		6.00e-
G01858	uncoupling protein 1, mitochondrial	345 95
		6.00e-
AAA85271.1	uncoupling protein	345 95
		5.00e-
P25874	UCP1_HUMAN Mitochondrial brown fat uncoupling protein 1 (UCP 1) (Thermogenin)	342 94
		5.00e-
CAA36214.1	uncoupling protein	342 94
		2.00e-
AAH08392.1	Similar to uncoupling protein 3 (mitochondrial, proton carrier)	214 55
AAK51556.1	AF371328_1 chondroadherin	627 e-179
AAH36360.1	Similar to chondroadherin	627 e-179
NP_001258.1	chondroadherin precursor	624 e-179
O15335	CHAD_HUMAN Chondroadherin precursor (Cartilage leucine-rich protein)	624 e-179
NM_007689		
NP_031715.1	Mm.8033 F:2.21	

NM_015734	AAC13410.1	chondroadherin	624 e-179
	CAB63072.1	dJ756G23.1 (novel Leucine Rich Protein)	234 2.00e-61
NP_056549.1	AAH08760.1	Similar to collagen, type V, alpha 1	629 e-179
	P20908	CA15_HUMAN Collagen alpha 1(V) chain precursor	629 e-179
	BAA14323.1	collagen alpha 1(V) chain precursor	629 e-179
	NP_000084.2	alpha 1 type V collagen preproprotein	629 e-179
	CGHU1V	collagen alpha 1(V) chain precursor	627 e-179
	AAA59993.1	pro-alpha-1 type V collagen	627 e-179
	AAF04726.1	collagen type XI alpha-a isoform B	495 e-139
	AAF04724.1	collagen type XI alpha-1	495 e-139
	AAF04725.1	collagen type XI alpha-1 isoform A	495 e-139
	NP_542196.1	alpha 1 type XI collagen isoform B preproprotein; collagen XI, alpha-1 polypeptide	493 e-138
	NP_542197.1	alpha 1 type XI collagen isoform C preproprotein; collagen XI, alpha-1 polypeptide	493 e-138
	NP_001845.2	alpha 1 type XI collagen isoform A preproprotein; collagen XI, alpha-1 polypeptide	493 e-138
NM_016896	Mm.15898		
	Q9WUL6		
Q9QY15	1	F:2.21	1419 0
	AAH35576.1	MAP3K14 protein	
		mitogen-activated protein kinase kinase kinase 14; serine/threonine protein-kinase	
	NP_003945.1		1414 0
		Mitogen-activated protein kinase kinase kinase 14 (NF-kappa beta-inducing kinase) (Serine/threonine protein kinase NIK) (HsNIK)	
NM_020266	Q99558		1414 0
	CAA71306.1	NIK, serine/threonine protein-kinase	1414 0
	CAA44969.2	HSJ1a protien	280 7e-075
	AAH47056.1	DNAJB2 protein	280 7e-075
Q9QY15	6	F:2.21	277 3e-074
	AAA09034.1	HSJ1a	

NM_009045 A37932	6	F:2.21	Mm.24996	NP_006727.2	DnaJ (Hsp40) homolog, subfamily B, member 2; heat shock protein, neuronal DNAJ-like 1	273 5e-073
				AAH11609.1	DnaJ (Hsp40) homolog, subfamily B, member 2	273 5e-073
				CAA44968.2	HSJ1b protein	273 5e-073
				AAP35751.1	DnaJ (Hsp40) homolog, subfamily B, member 2	273 5e-073
				P25686	DnaJ homolog subfamily B member 2 (Heat shock 40 kDa protein 3)	
				S23508	(DnaJ protein homolog 1) (HSJ-1)	273 5e-073
				AAA09035.1	dnaJ protein homolog - human	271 2e-072
				HSJ1b		271 2e-072
				Q04206	Transcription factor p65 (Nuclear factor NF-kappa-B p65 subunit)	929 0
				A40851	transforming protein (rel) homolog - human	929 0
				AAA36408.1	NF-kappa-B transcription factor	929 0
				A42017	transcription factor NF-kappa-B chain p65 - human	925 0
				CAA80524.2	p65 subunit of transcription factor NF-kappaB	925 0
					v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65; v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65))	889 0
				NP_068810.1	enhancer in B-cells 3 (p65))	889 0
				I53719	NF-kappa-B transcription factor subunit - human	889 0
				AAA20946.1	NF-kappa-B transcription factor subunit	889 0
				2006293A	transcription factor NF-kappa B	889 0
					v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	889 0
				AAR13863.1	p65 (avian)	609 e-174
				1NF1JA	Chain A, I-Kappa-B-AlphaNF-Kappa-B Complex	609 e-174
				1NF1JC	Chain C, I-Kappa-B-AlphaNF-Kappa-B Complex	609 e-174

AAH14095.1	RELA protein	457 e-128
AAH11603.1	RELA protein	446 e-124
NP_002899.1	v-rel reticuloendotheliosis viral oncogene homolog; oncogene REL,	
Q04864	avian reticuloendotheliosis; C-Rel proto-oncogene protein	375 e-103
A60646	C-Rel proto-oncogene protein (C-Rel protein)	375 e-103
CAA52954.1	transforming protein (c-rel) - human	375 e-103
	c-rel	375 e-103
	reticuloendotheliosis viral oncogene homolog B; v-rel avian	
	reticuloendotheliosis viral oncogene homolog B (nuclear	
	factor of kappa light polypeptide gene enhancer in	
	B-cells 3)	
NP_006500.2		312 1e-084
AAC82346.1	I-REL	312 1e-084
AAH28013.1	Reticuloendotheliosis viral oncogene homolog B	312 1e-084
Q01201	Transcription factor RelB (I-Rel)	307 5e-083
A42617	66K rel-related protein I-rel - human	307 5e-083
AAA36127.1	I-Rel	307 5e-083
	ATP-binding cassette, sub-family C, member 1 isoform 1; multiple drug	
	resistance-associated protein; multiple drug resistance	
	protein 1; multidrug resistance protein	
NM_008576	Mm.19663	2623 0
NP_032602.1	F:2.21	2623 0
NP_004987.1	Multidrug resistance-associated protein 1	2623 0
P33527	multidrug resistance-associated protein	2619 0
AAB46616.1	multidrug resistance protein (cell line H69AR) - human	2590 0
DVHUAR	multidrug resistance protein	
AAB83979.1	ATP-binding cassette, sub-family C, member 1 isoform 6; multiple drug	
	resistance-associated protein; multiple drug resistance	
	protein 1; multidrug resistance protein	
NP_063956.1		2536 0

			ATP-binding cassette, sub-family C, member 1 isoform 7; multiple drug resistance-associated protein; multiple drug resistance protein 1; multidrug resistance protein	2520	0
			ATP-binding cassette, sub-family C, member 1 isoform 3; multiple drug resistance-associated protein; multiple drug resistance protein 1; multidrug resistance protein	2476	0
			multidrug resistance protein	2444	0
			ATP-binding cassette, sub-family C, member 1 isoform 5; multiple drug resistance-associated protein; multiple drug resistance protein 1; multidrug resistance protein	2442	0
			multidrug resistance protein	2409	0
			ATP-binding cassette, sub-family C, member 3 isoform MRP3; canicular multispecific organic anion transporter	1656	0
			Canalicular multispecific organic anion transporter 2 (Multidrug resistance-associated protein 3) (Multi-specific organic anion transporter-D) (MOAT-D)	1656	0
			multidrug resistance-associated protein 3	1656	0
			ABC transporter MOAT-D	1656	0
AK011815				623 e-178	
BAC36873	N/A	F:2.2	unnamed protein product	341 2e-093	
NM_008064			unnamed protein product		
P70699	Mm.4793	F:2.2	GAA protein	1559	0
			alpha-glucosidase (EC 3.2.1.20) precursor, lysosomal - human	1559	0
			acid alpha-glucosidase	1559	0
			acid alpha-glucosidase	1559	0
			acid alpha-glucosidase preproprotein; lysosomal alpha-glucosidase; acid maltase	1559	0
			NP_000143.1		

P10253	Lysosomal alpha-glucosidase precursor (Acid maltase)	1559	0
CAA68763.1	glucan 1, 4-alpha-glucosidase	1559	0
CAA68764.1	70 kD alpha-glucosidase	1302	0
	MGA_HUMAN Maltase-glucoamylase, intestinal [Includes: Maltase (Alpha-glucosidase); Glucoamylase (Glucan 1,4-alpha-glucosidase)]		
O43451		747	0
AAC39568.2	maltase-glucoamylase	747	0
NP_004659.1	maltase-glucoamylase; brush border hydrolase; alpha-glucosidase	745	0
AAL83560.1	maltase-glucoamylase	724	0
NP_001032.1	sucrase-isomaltase	717	0
P14410	Sucrase-isomaltase, intestinal [Contains: Sucrase; Isomaltase]	717	0
	sucrose alpha-glucosidase (EC 3.2.1.48) / oligo-1, 6-glucosidase (EC 3.2.1.10) [validated] - human		
UUHU		717	0
CAA45140.1	prosucrose-isomaltase	717	0
XP_374541.1	similar to maltase-glucoamylase	589	e-168
AAA60551.1	sucrase-isomaltase	531	e-150
	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1; ATPase II; aminophospholipid translocase		
NM_009727			
NP_033857.1			
	Potential phospholipid-transporting ATPase IA (Chromaffin granule ATPase II) (ATPase class I type 8A member 1)	2206	0
Q9Y2Q0		2206	0
AAD34706.1	ATPase II	2206	0
BAA77248.1	ATPasell	2197	0
BAC86905.1	unnamed protein product	1575	0
	Potential phospholipid-transporting ATPase IB (ATPase class I type 8A member 2) (ML-1)		
Q9NTI2		1568	0
CAD97848.1	hypothetical protein	1357	0
BAC86402.1	unnamed protein product	1285	0
BAC04396.1	unnamed protein product	1062	0

NM_019547	S38384	Mm.3865	F:2.2	T46328	probable adenosinetriphosphatase (EC 3.6.1.3) DKFZp434B1913.1		
				CAB70658.1	[similarity] - human (fragment)	984	0
NM_019547	S38384	Mm.3865	F:2.2	P98198	hypothetical protein	984	0
				NP_065185.1	Potential phospholipid-transporting ATPase ID (ATPase class I type 8B member 2)	822	0
NM_019547	S38384	Mm.3865	F:2.2	AAQ19027.1	ATPase, Class I, type 8B, member 2	821	0
				NP_059965.2	possible aminophospholipid translocase ATP8B2	821	0
NM_019547	S38384	Mm.3865	F:2.2	S38382	RNA-binding region containing protein 1 isoform a; ssDNA binding	352 9e-097	
				CAA53063.1	protein SEB4; CLL-associated antigen KW-5	327 3e-089	
NM_019547	S38384	Mm.3865	F:2.2	Q9H0Z9	SEB4D protein - human (fragment)	327 3e-089	
				CAC21462.1	SEB4D	326 7e-089	
NM_019547	S38384	Mm.3865	F:2.2	AAH18711.1	RNA-binding region containing protein 1 (HSRNASEB) (ssDNA binding	326 7e-089	
				AAL99924.1	protein SEB4) (CLL-associated antigen KW-5)	326 7e-089	
NM_019547	S38384	Mm.3865	F:2.2	S38383	dJ800J21.2.1 (ssDNA binding protein SEB4D (HSRNASEB), isoform 1)	312 1e-084	
				CAA53064.1	RNPC1 protein	312 1e-084	
NM_019547	S38384	Mm.3865	F:2.2	CAC36889.1	CLL-associated antigen KW-5	239 1e-062	
				BAC04474.1	SEB4B protein - human (fragment)	223 1e-057	
NM_019547	S38384	Mm.3865	F:2.2	CAC32281.1	SEB4B	219 2e-056	
				CAC32282.1	dJ259A10.1 (ssDNA binding protein (SEB4D))	209 1e-053	
NM_019547	S38384	Mm.3865	F:2.2	NP_002151.1	unnamed protein product	2595	0
					tenascin C (hexabrachion); Hexabrachion (tenascin); hexabrachion		
NM_019547	S38384	Mm.3865	F:2.2		tenascin C, cytotactin		
					Tenascin precursor (TN) (Hexabrachion) (Cytotactin) (Neuronection)		
NM_019547	S38384	Mm.3865	F:2.2		(GMEM) (JI) (Miotendinous antigen)		
					(Glioma-associated-extracellular matrix antigen) (GP		
NM_019547	S38384	Mm.3865	F:2.2	P24821	150-225) (Tenascin-C) (TN-C)	2595	0
				A32160	tenascin-C - human	2595	0

AF072403	Mm.27503	CAA55309.1	human tenascin-C	2595	0
O08584	F:2.2	AAA88083.1	hexabrachion	2593	0
		CAA39628.1	tenascin	2591	0
		AAA52703.1	hexabrachion	1776	0
		A40701	tenascin-X precursor - human	863	0
		CAB89296.1	dJ34F7.1.1 (tenascin XB (isoform 1))	860	0
		NP_061978.4	tenascin XB isoform 1; tenascin XB1; tenascin XB2; hexabrachion-like	858	0
		P22105	Tenascin X precursor (TN-X) (Hexabrachion-like)	858	0
		AAB47488.1	tenascin X	858	0
		AAB67981.1	tenascin X	713	0
		NP_003276.2	tenascin R (restrictin, janusin)	629	e-179
		CAA91947.1	tenascin-R (restrictin)	629	e-179
		CAA66709.1	tenascin-R	628	e-179
		AAC23699.1	DNA-binding protein CPBP	449	e-126
			core promoter element binding protein; B-cell derived 1; B		
			cell-derived 1; prostate adenocarcinoma-1; suppression		
			of tumorigenicity 12 (prostate); protooncogene BCD1;		
		NP_001291.3	kruppel-like factor 6	444	e-124
			Core promoter element-binding protein (Kruppel-like factor 6)		
			(B-cell derived protein 1) (Proto-oncogene BCD1)		
			(Transcription factor Zf9) (GC-rich sites binding factor		
		Q99612	GBF)	444	e-124
		BAA33050.1	DNA-binding zinc finger(GBF)	444	e-124
		AAH00311.1	Core promoter element binding protein	444	e-124
		AAM73548.1	Core promoter element binding protein	444	e-124
		AAP35424.1	Core promoter element binding protein	444	e-124
		AAC39929.1	Kruppel-like zinc finger protein Zf9	442	e-124
		JE0235	HIV-promoter GC-rich sites binding factor - human	442	e-124

AAH04301.1	COPEB protein	392	e-109
CAD97885.1	hypothetical protein	204	2e-052
	Kruppel-like factor 7 (ubiquitous); ubiquitous Kruppel-like		
NP_003700.1	transcription factor	204	2e-052
O75840	Krueppel-like factor 7 (Ubiquitous krueppel-like factor)	204	2e-052
BAA33521.1	ubiquitous Kruppel like factor	204	2e-052
NM_008908			6.00e-
NP_032934.1	peptidylprolyl isomerase C (cyclophilin C)	345	95
	CYPC_HUMAN Peptidyl-prolyl cis-trans isomerase C (PPIase) (Rotamase)		6.00e-
P45877	(Cyclophilin C)	345	95
			6.00e-
A54204	peptidylprolyl isomerase (EC 5.2.1.8) C precursor	345	95
			6.00e-
AAB31350.1	cyclophilin C; Cyp-C	345	95
			6.00e-
AAH02678.1	peptidylprolyl isomerase C (cyclophilin C)	345	95
	CYPB_HUMAN Peptidyl-prolyl cis-trans isomerase B precursor (PPIase) (Rotamase)		7.00e-
P23284	(Cyclophilin B) (S-cyclophilin) (SCYLP) (CYP-S1)	269	72
			7.00e-
CSHUB	peptidylprolyl isomerase (EC 5.2.1.8) B precursor	269	72
			7.00e-
AAA52150.1	cyclophilin B	269	72
			7.00e-
AAA35733.1	cyclophilin	269	72
			7.00e-
NP_000933.1	peptidylprolyl isomerase B (cyclophilin B)	269	72
			7.00e-
AAA36601.1	secreted cyclophilin-like protein	269	72

[illegible]

O94832	Myosin Id	649	0
BAA34447.2	KIAA0727 protein	649	0
XP_050041.6	myosin ID	618	e-176
XP_353586.1	similar to Myosin Id (Myosin heavy chain myr 4)	605	e-172
XP_374431.1	similar to myosin IG	605	e-172
XP_291223.2	myosin IG	604	e-172
AK003918			
BAB23076.1	Mm.29997 F:2.18	513	e-145
NP_065701.2	reticulocalbin-like; reticulocalbin	513	e-145
AAH13436.1	hypothetical protein LOC57333	513	e-145
AAO43054.1	reticulocalbin-like protein RLP49 precursor	513	e-145
AAG09692.1	AF183423_1 reticulocalbin precursor	512	e-145
1.00e-			
NP_002892.1	reticulocalbin 1 precursor; Rcal; Reticulocalbin 1	327	89
1.00e-			
Q15293	RCN1_HUMAN Reticulocalbin 1 precursor	327	89
1.00e-			
JC4173	reticulocalbin precursor	327	89
1.00e-			
BAA07670.1	reticulocalbin	327	89
1.00e-			
AAH10120.1	reticulocalbin 1, EF-hand calcium binding domain	327	89
1.00e-			
2112269A	reticulocalbin	327	89
3.00e-			
AAK72908.1	calumenin	293	79
4.00e-			
AAF76141.1	crocalbin-like protein	293	79
2.00e-			
NP_001210.1	calumenin precursor	287	77

O43852	CALU_HUMAN Calumenin precursor (IEF SSP 9302)	287	77	2.00e-
AAC17216.1	calumein	287	77	2.00e-
AAH13383.1	calumenin	287	77	2.00e-
AAB97725.1	calumenin	286	77	5.00e-
NM_009381 NP_033407.1 Mm.28585 F:2.18	thyroid hormone responsive (SPOT14 homolog, rat); Thyroid hormone responsive	221	58	4.00e-
	SPOT14, rat, homolog of; thyroid hormone responsive SPOT14 (rat) homolog	221	58	4.00e-
	THIH_HUMAN Thyroid hormone-inducible hepatic protein (Spot 14 protein) (SPOT14)	221	58	4.00e-
	(S14 protein)	221	58	4.00e-
CAA69685.1	Spot14 protein	221	58	4.00e-
AAH31989.1	thyroid hormone responsive (SPOT14 homolog, rat)	221	58	4.00e-
NP_003485.1	dysferlin; dystrophy-associated fer-1-like 1	2974	0	0
Dysferlin (Dystrophy associated fer-1-like protein) (Fer-1 like protein 1)				
O75923	protein 1)	2974	0	0
AAC63519.1	dysferlin	2974	0	0
BAB84930.1	FLJ00175 protein	2790	0	0
CAA07603.1	LGMD2B protein	2667	0	0
NP_038479.1	myoferlin isoform a; fer-1-like 3	2016	0	0
Q9NZM1	Myoferlin (Fer-1 like protein 3)	2016	0	0
AAF27176.1	myoferlin	2016	0	0
BAA86521.2	KIAA1207	2016	0	0
NP_579899.1	myoferlin isoform b; fer-1-like 3	2015	0	0

NIM_016749	Mm.26962			AAG23737.1	fer-1 like protein 3	2013	0
P70402	1	F-2.18		AAF27177.1	myoferlin	1983	0
				T12449	hypothetical protein DKFZp564E1616.1 - human (fragments)	1696	0
				CAB46370.1	hypothetical protein	1696	0
				AAH52617.1	FER1L3 protein	867	0
				XP_031009.3	similar to Fer1l3 protein	686	0
				AAH44226.1	Myosin binding protein H	793	0
				Q13203	Myosin-binding protein H (MyBP-H) (H-protein)	793	0
				AAB86737.1	myosin binding protein H	784	0
				NP_004988.1	myosin binding protein H; myosin-binding protein H	775	0
				A46118	myosin-binding protein H - human	775	0
					fibronectin type III domains, aa 70-170 and aa 265-365; immunoglobulin C2 domains, aa 185-264 and aa 391-473; 86 kD protein	775	0
				XP_291485.3	similar to Myosin-binding protein H (MyBP-H) (H-protein)	469	e-132
				NP_004524.1	fast-type; fast-type muscle myosin-binding-protein C	562	e-130
				Q14324	skeletal muscle fast-isoform	562	e-130
				S36845	myosin-binding protein C, fast-type muscle - human	562	e-130
				CAA51544.1	fast MyBP-C	562	e-130
				NP_002456.1	slow-type; skeletal muscle C-protein	459	e-129
				S36846	myosin-binding protein C, slow-type muscle - human	459	e-129
				CAA51545.1	slow MyBP-C	459	e-129
				CAD38625.1	hypothetical protein	458	e-128
				CAD91144.1	hypothetical protein	458	e-128
				CAD38925.1	hypothetical protein	457	e-128

[illegible]

NM_019803	NP_001837.1	alpha 2 type IV collagen preproprotein; canstatin	474 e-134
	CAA29098.1	alpha (2) chain	474 e-134
	AA58422.1	collagen alpha-2 type IV	473 e-133
	AAA52043.1	alpha-2 type IV collagen	471 e-133
	Q14031	CA64_HUMAN Collagen alpha 6(IV) chain precursor	380 e-106
	AAB19038.1	collagen type IV a6 chain	380 e-106
		type IV alpha 6 collagen isoform A precursor; collagen IV, alpha-6 polypeptide;	
	NP_001838.1	collagen of basement membrane, alpha-6	380 e-106
	CGHU6B	collagen alpha 6(IV) chain precursor	380 e-106
	AAA19569.2	A type IV collagen	380 e-106
NM_080551.1	NP_003334.2	ubiquitin-conjugating enzyme E2G 2 isoform 1; ubiquitin conjugating enzyme 7; ubiquitin conjugating enzyme G2; ubiquitin carrier protein G2; ubiquitin-protein ligase G2	343 8e-094
		Ubiquitin-conjugating enzyme E2 G2 (Ubiquitin-protein ligase G2)	
	P56554	(Ubiquitin carrier protein G2)	343 8e-094
	CAB90551.1	human ubiquitin conjugating enzyme G2 EC 6.3.2.19.	343 8e-094
	AAH01738.1	Ubiquitin-conjugating enzyme E2G 2, isoform 1	343 8e-094
	AAH08351.1	Ubiquitin-conjugating enzyme E2G 2, isoform 1	343 8e-094
	AAH11569.1	Ubiquitin-conjugating enzyme E2G 2, isoform 1	343 8e-094
	AAP35560.1	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	343 8e-094
	AAC32312.1	ubiquitin conjugating enzyme G2	327 4e-089
		ubiquitin-conjugating enzyme E2G 2 isoform 2; ubiquitin conjugating enzyme 7; ubiquitin conjugating enzyme G2; ubiquitin carrier protein G2; ubiquitin-protein ligase G2	288 2e-077
NM_011100	NP_872630.1	carrier protein G2; ubiquitin-protein ligase G2	694 0
	NP_002722.1	protein kinase, cAMP-dependent, catalytic, beta isoform b	694 0
	P22694	cAMP-dependent protein kinase, beta-catalytic subunit (PKA C-beta)	694 0
	OKHUCB	protein kinase (EC 2.7.1.37), cAMP-dependent, beta catalytic chain - human	694 0

AAA60170.1	cAMP-dependent protein kinase catalytic subunit	694	0
AAH35058.1	PRKACB protein	688	0
NP_891993.1	protein kinase, cAMP-dependent, catalytic, beta isoform a	671	0
CAD97818.1	hypothetical protein	671	0
CAE46017.1	hypothetical protein	671	0
NP_002721.1	protein kinase, cAMP-dependent, catalytic, alpha	661	0
P17612	cAMP-dependent protein kinase, alpha-catalytic subunit (PKA C-alpha)	661	0
	protein kinase (EC 2.7.1.37), cAMP-dependent, alpha catalytic chain -		
OKHU2C	human	661	0
CAA30597.1	unnamed protein product	661	0
AAH39846.1	Protein kinase, cAMP-dependent, catalytic, alpha	661	0
	protein kinase (EC 2.7.1.37), cAMP-dependent, gamma catalytic chain -		
OKHUCG	human		
AAC41690.1	protein kinase A gamma-subunit	578	e-164
	protein kinase, cAMP-dependent, catalytic, gamma; PKA C-gamma;		
NP_002723.2	serine(threonine) protein kinase	575	e-163
P22612	cAMP-dependent protein kinase, gamma-catalytic subunit (PKA C-gamma)	575	e-163
CAA04863.1	cAMP-dependent protein kinase gamma isoform	575	e-163
AAH39888.1	Protein kinase, cAMP-dependent, catalytic, gamma	574	e-163
AAH16285.1	PRKACB protein	504	e-142
NP_005035.1	protein kinase, X-linked	375	e-103
P51817	Serine/threonine protein kinase PRKX (Protein kinase PKX1)	375	e-103
I38121	protein kinase - human	375	e-103
CAA59733.1	protein kinase	375	e-103
AAH41073.1	Protein kinase, X-linked	375	e-103
	protein kinase (EC 2.7.1.37), cAMP-dependent, alpha catalytic		
A38143	chain, short splice form - human (fragment)	363	1e-099
AAA60094.1	protein kinase A-alpha	363	1e-099

Q32XAVI (125.1)
AAK3E161 1 AE316824 1 asenotin precursors

NIM_007682 P27790	Mm.41454 F:2.15	NP_001911.1	decorin isoform a preproprotein; dermatan sulphate proteoglycans II; bone proteoglycan II; proteoglycan core protein	395 e-109
		NP_598010.1	decorin isoform a preproprotein; dermatan sulphate proteoglycans II; bone proteoglycan II; proteoglycan core protein	395 e-109
		P07585	PGS2_HUMAN Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40)	395 e-109
		NBHUC8	decorin precursor	395 e-109
		AAB00774.1	proteoglycan core protein	395 e-109
		AAD44713.1	decorin variant A	395 e-109
		AAH05322.1	decorin	395 e-109
		AAL92176.1	AF491944_1 decorin	395 e-109
		AAA52301.1	decorin	375 e-103
				4.00e-
		BAA90967.1	unnamed protein product	244 64
			decorin isoform b precursor; dermatan sulphate proteoglycans II; bone proteoglycan II; proteoglycan core protein	4.00e-
		NP_598011.1		218 56
				4.00e-
		AAF61437.1	decorin B	218 56
				1.00e-
		BAB55060.1	unnamed protein product	209 53
			centromere protein B; centromere protein B (80kD); centromere autoantigen B	828 0
		NP_001801.1	Major centromere autoantigen B (Centromere protein B) (CENP-B)	828 0
		P07199	centromere protein B - human	828 0
		S18735	centromere protein B (CENP-B)	828 0
		CAA38879.1	centromere autoantigen B (80KDa)	828 0
		CAC17547.1	dJ1009E24.5 (Centromere protein B (80KDa))	828 0
		AAH53847.1	Centromere protein B	828 0
		AAB21673.1	major centromere protein, CENP-B [human, Peptide, 594 aa]	828 0
		CAA28918.1	CENP-B	822 0

Chain A, Crystal Structure Of Cenp-B(1-129) Complexed With The			
	1HLVJA	Cenp- B Box Dna	244 7e-064
	AAB70165.1	centromere protein B; CENP-B	236 2e-061
NM_010728			
NP_034858.1	Mm.172		
	F:2.13		
	NP_002308.2	lysyl oxidase preproprotein; protein-lysine 6-oxidase	649 0
	P28300	LYOX_HUMAN Protein-lysine 6-oxidase precursor (Lysyl oxidase)	649 0
	AAD02130.1	lysyl oxidase	649 0
	AAA59525.1	lysyl oxidase	649 0
	AAB23549.1	lysyl oxidase	649 0
	AAK58603.1	AF270645_1 lysyl oxidase	648 0
	OXHUL	protein-lysine 6-oxidase (EC 1.4.3.13) precursor	647 0
	AAB21243.1	lysyl oxidase	638 0
			2.00e-
	AAH15090.1	lysyl oxidase-like 1	352 96
			2.00e-
	NP_005567.1	lysyl oxidase-like 1	352 96
			2.00e-
	Q08397	LOL1_HUMAN Lysyl oxidase homolog 1 precursor (Lysyl oxidase-like protein 1) (LOL)	352 96
			2.00e-
	A48501	probable protein-lysine 6-oxidase (EC 1.4.3.13) precursor	352 96
			2.00e-
	AAA50162.1	lysyl oxidase-like protein	352 96
			2.00e-
	AAA68940.1	lysyl oxidase-like protein	352 96
			5.00e-
	AAH33130.1	Similar to lysyl oxidase-like 4	225 58
			5.00e-
	AAK91134.1	AF284815_1 lysyl oxidase-like protein	225 58

NP_115992.1	lysyl oxidase-like 3				225	58	5.00e-
P58215	LOL3_HUMAN Lysyl oxidase homolog 3 precursor (Lysyl oxidase-like protein 3)				225	58	5.00e-
AAK51671.1	AF282619_1 lysyl oxidase-like 3 protein				225	58	5.00e-
AAK63205.1	AF311313_1 lysyl oxidase-like 3 protein				225	58	5.00e-
AK018470		Mm.13691					
S59069	NP_071927.1 zinc finger protein 336; GDNF-inducible zinc finger gene 1	3	F:2.13		962	0	
	Q9H116 Zinc finger protein 336				962	0	
	CAC03438.2 dJ322G13.2.3 (zinc finger protein FLJ21794, isoform 3)				962	0	
	BAC98464.1 GDNF-inducible zinc finger protein 1				962	0	
	BAB71107.1 unnamed protein product				894	0	
	CAC17422.1 dJ322G13.2.1 (zinc finger protein FLJ21794, isoform 1)				688	0	
	CAC34610.1 dJ322G13.2.2 (zinc finger protein FLJ21794, isoform 2)				498	e-176	
	BAB15134.1 unnamed protein product				475	e-133	
	NP_149350.1 DKFZP572C163 protein				280	9e-075	
	BAB14145.1 unnamed protein product				280	9e-075	
	T14757 hypothetical protein DKFZp572C163.1 - human (fragment)				280	9e-075	
	CAB53677.1 hypothetical protein				280	9e-075	
	XP_372091.1 similar to DKFZP572C163 protein				278	3e-074	
	XP_372096.1 similar to DKFZP572C163 protein				278	3e-074	
	BAC04610.1 unnamed protein product				278	3e-074	
	Q9UJU3 Zinc finger protein 228				274	5e-073	
	AAF12816.1 zinc finger protein ZNF228				274	5e-073	
NM_010500							
NP_034630.1	NP_057629.1 immediate early response 5	Mm.12246	F:2.13		276	7e-074	
	AAF44348.1 hypothetical protein SBB148				276	7e-074	

NIM_008244	AAH00128.1	Immediate early response 5	276 7e-074
	AAG23784.1	PP4583	275 3e-073
	CAB91983.1	hypothetical protei	274 4e-073
		hepatocyte growth factor-regulated tyrosine kinase substrate; human	
I49759	Mm.7919	F:2.13	
	NP_004703.1	growth factor-regulated tyrosine kinase substrate	1264 0
	BAA23366.1	Hrs	1264 0
	AAC51929.1	hepatocyte growth factor-regulated tyrosine kinase substrate	1264 0
	AAH03565.1	hepatocyte growth factor-regulated tyrosine kinase substrate	1264 0
	AAP88756.1	hepatocyte growth factor-regulated tyrosine kinase substrate	1264 0
AK012765	AAF82361.1	isoform 2	1034 0
	BAA12106.2	expressed ubiquitously with strong expression in brain	765 0
	NP_055581.2	KIAA0193 gene product	758 0
	AAH40492.1	Unknown (protein for MGC:33750)	758 0
	Q12765	Y193_HUMAN Hypothetical protein KIAA0193	642 0
NIM_008305	NP_612364.1	hypothetical protein BC002980	436 e-122
	AAH17317.1	Unknown (protein for MGC:29622)	436 e-122
	AAH10408.1	Unknown (protein for IMAGE:3945715)	435 e-122
	AAH02980.1	Similar to KIAA0193 gene product	409 e-114
	AAH20564.2	Similar to hypothetical protein MGC29406	385 e-107
		Basement membrane-specific heparan sulfate proteoglycan core protein	
S18252	Mm.27366		
	2	F:2.12	
	P98160	precursor (HSPG) (Perlecan) (PLC)	4197 0
	A38096	perlecan precursor - human	4196 0
	AAA52700.1	heparan sulfate proteoglycan	4196 0
	CAC18534.1	heparan sulfate proteoglycan perlecan	4190 0
NIM_008305		heparan sulfate proteoglycan of	
		basement membrane; endorepellin (domain V region);	
S18252	NP_005520.2	perlecan	4172 0

CAA44373.1			Human basement membrane heparan sulfate proteoglycan core protein	4172	0
AAB21121.2			heparan sulfate proteoglycan core protein; HSPG	940	0
AAA52699.1			heparan sulfate proteoglycan	868	0
NP_114141.1			hemiscentin; fibulin 6	358	9e-098
XP_175125.4			hemiscentin-2	356	6e-097
P24043			Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy chain)	350	4e-095
CAA81394.1			laminin M chain (merosin)	350	4e-095
AK014649					
BAB29488.1	Mm.27589	F:2.12	NP_919417.1 D-lactate dehydrogenase isoform 2 precursor; D-lactate dehydrogenase	738	0
			NP_705690.2 D-lactate dehydrogenase isoform 1 precursor; D-lactate dehydrogenase	728	0
			AAH47902.1 LDHD protein	728	0
			AAM50322.1 D-lactate dehydrogenase	646	0
NM_007679					5.00e-
NP_031705.1	Mm.4639	F:2.11	CCAAT/enhancer binding protein delta	346	95
			CEBD_HUMAN CCAAT/enhancer binding protein delta (C/EBP delta) (Nuclear factor		3.00e-
			NP_49716 NF-IL6-beta) (NF-IL6-beta)	343	94
					3.00e-
			A47008 transcription activator NF-IL6 beta	343	94
					3.00e-
			AAB27293.1 CCAAT/enhancer-binding protein delta; C/EBP delta	343	94
					4.00e-
			AAA59927.1 NF-IL6-beta protein	340	93
			SH3 domain binding glutamic acid-rich protein like; SH3-binding domain glutamic		3.00e-
			NP_003013.1 acid-rich protein like	204	52
					3.00e-
NM_019989	Mm.19645				
NP_064373.1	1	F:2.1	SH3L_HUMAN SH3 domain-binding glutamic acid-rich-like protein	204	52
					3.00e-
			JE0178 SH3 binding glutamate-rich protein	204	52

Accession	Gene	Protein	Length	Score
AAC27445.1	SH3 domain binding glutamic acid-rich-like protein		204	3.00e-52
AAH16709.1	SH3 domain binding glutamic acid-rich protein like		204	3.00e-52
CAB66652.1	hypothetical protein		202	1.00e-51
NP_004435.3	ephrin receptor EphB4 precursor; hepatoma transmembrane kinase Ephrin type-B receptor 4 precursor (Tyrosine-protein kinase receptor P54760 HTK)		1773	0
A54092	protein-tyrosine kinase (EC 2.7.1.112) htk precursor - human		1773	0
AAK21010.1	ephrin type-B receptor 4 precursor		1773	0
AAL14194.1	receptor protein tyrosine kinase EphB4		1773	0
AAH52804.1	Ephrin receptor EphB4, precursor		1771	0
AAA20598.1	tyrosine kinase		1760	0
AAL14195.1	receptor protein tyrosine kinase variant EphB4v1		1646	0
AAH04264.1	Similar to EphB4		1540	0
NP_004434.2	ephrin receptor EphB3 precursor; EPH-like tyrosine kinase-2; human embryo kinase 2		1085	0
AAH52968.1	Ephrin receptor EphB3, precursor		1085	0
P54753	Ephrin type-B receptor 3 precursor (Tyrosine-protein kinase receptor HEK-2)		1082	0
S37627	protein-tyrosine kinase (EC 2.7.1.112), receptor-type - human		1082	0
CAA53021.1	protein tyrosine kinase-receptor		1082	0
BAA06506.1	tyrosine kinase precursor		1058	0
NP_059145.1	ephrin receptor EphB2 isoform 1 precursor; developmentally-regulated eph-related tyrosine kinase; elk-related tyrosine kinase;		1051	0
AAB94602.1	ephrin tyrosine kinase 3		1051	0
	protein-tyrosine kinase EPHB2v			

Ephrin type-B receptor 2 precursor (Tyrosine-protein kinase receptor EPH-3) (DRT) (Receptor protein-tyrosine kinase HEK5)			P29323			1051	0
(ERK)							
NM_010128	Mm.18278						
P47801	5	F:2.09	NP_001414.1	epithelial membrane protein 1		221	4e-057
				Epithelial membrane protein-1 (EMP-1) (Tumor-associated membrane protein) (CL-20) (B4B protein)		221	4e-057
			P54849			221	4e-057
			CAA90627.1	B4B		221	4e-057
			CAA69217.1	progression associated protein		221	4e-057
			AAC51207.1	epithelial membrane protein		221	4e-057
			AAC51783.1	TMP		221	4e-057
			AAH47300.1	Epithelial membrane protein 1		221	4e-057
			G02355	tumor-associated membrane protein TMP - human		220	9e-057
NM_025757	Mm.28754						
NP_080033.1	8	F:2.09	NP_076957.3	hypothetical protein MGC3048		426	e-118
			AAH41829.1	Hypothetical protein MGC3048		426	e-118
			AAH00636.2	MGC3048 protein		426	e-118
			BAB85036.1	unnamed protein product		423	e-117
NM_020271							
NP_064667.1	Mm.29410	F:2.08	NP_064711.1	hypothetical protein dJ37E16.5		212	e-106
			AAH00320.1	hypothetical protein dJ37E16.5		212	e-106
						2.00e-	
			AAH09756.1	Similar to hypothetical protein dJ37E16.5 sialyltransferase 4A;		212	68
				CMP-N-acetylneuraminate-beta-galactosamide-alpha-2, 3-sialyltransferase; sialyltransferase 4A			
				(beta-galactoside alpha-2,3-sialyltransferase); alpha			
				2,3-ST; Gal-beta-1,3-GalNAc-alpha-2,3-sialyltransferase			
NM_009177	Mm.24833						
P54751	4	F:2.08	NP_003024.1			562	e-160

sialyltransferase 4A;		
CMP-N-acetylneuraminase-beta-galactosamide-alpha-2,		
3-sialyltransferase; sialyltransferase 4A		
(beta-galactoside alpha-2,3-sialyltransferase); alpha		
2,3-ST; Gal-beta-1,3-GalNAc-alpha-2,3-sialyltransferase		
NP_775479.1	CMP-N-acetylneuraminase-beta-galactosamide-alpha-2,	562 e-160
3-sialyltransferase (Beta-galactoside		
alpha-2,3-sialyltransferase) (Alpha 2,3-ST) (Gal-NAc6S)		
(Gal-beta-1,3-GalNAc-alpha-2,3-sialyltransferase)		
(ST3GalIA) (ST3O) (ST3GalA.1) (SIAT4-A) (ST3Gal I)		
Q11201	(SIATFL)	562 e-160
I54229	beta-galactoside alpha-2,3-sialyltransferase (EC 2.4.99.4) - human	562 e-160
AAC37574.1	beta-galactoside alpha-2,3-sialyltransferase	562 e-160
AAH18357.1	Sialyltransferase 4A	562 e-160
AAA36612.1	sialyltransferase	562 e-160
AAC17874.1	alpha-2,3-sialyltransferase	559 e-159
sialyltransferase 4B; sialyltransferase 4B (beta-galactoside		
alpha-2,3-sialyltransferase); alpha 2,3-ST;		
Gal-beta-1,3-GalNAc-alpha-2,3-sialyltransferase;		
CMP-N-acetylneuraminase-beta-galactosamide-alpha-2,		
3-sialyltransferase		
NP_008858.1	CMP-N-acetylneuraminase-beta-galactosamide-alpha-2,	332 2e-090
3-sialyltransferase (Beta-galactoside		
alpha-2,3-sialyltransferase) (Alpha 2,3-ST) (Gal-NAc6S)		
(Gal-beta-1,3-GalNAc-alpha-2,3-sialyltransferase)		
Q16842	(ST3GalA.2) (SIAT4-B) (ST3Gal II)	332 2e-090
JC5251	beta-galactoside alpha-2,3-sialyltransferase (EC 2.4.99.4) - human	332 2e-090

NM_010052	Mm.15706	CAA65447.1	beta-galactoside alpha-2,3-sialyltransferase	332	2e-090
NP_034182.1	9	AAB40389.1	Gal beta-1,3 GalNAc alpha-2,3 sialyltransferase	332	2e-090
		AAH36777.1	Sialyltransferase 4B	332	2e-090
		CAA78163.1	putative homeotic protein	578	0
	F:2.07	AAH13197.1	Unknown (protein for MGC:17291)	573	0
			DLK_HUMAN Delta-like protein precursor (DLK) (pG2) [Contains: Fetal antigen 1 (FA1)]	572	0
		S53716	delta-like homeotic protein dlk, long splice form precursor	572	0
		NP_003827.2	delta-like homolog	572	0
		AAH07741.1	Similar to delta-like homolog (Drosophila)	572	0
		AAH14015.1	Unknown (protein for MGC:20310)	572	0
		AAA75364.1	dlk gene product	572	0
		2109224A	dlk gene	572	0
			alternatively spliced; lacking 219 bp between positions 858 and 859; The 219 bp deletion has been demonstrated to originate by alternative splicing within an exon	424	e-118
		AAA75365.1	dlk gene	424	e-118
		2109224C	dlk gene	6.00e-	
		S71548	homeotic protein pG2	171	84
				2.00e-	
		CAA35582.1	unidentified reading frame (AA 1-286)	171	83
			DLL1_HUMAN Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta1)	9.00e-	
		O00548	(H-Delta-1)	226	59
				9.00e-	
		AAB61286.1	Delta	226	59
				9.00e-	
		AAG09716.1	AF222310_1 Delta1	226	59
				9.00e-	
		NP_005609.2	delta-like 1; delta-like 1 (mouse) homolog; delta-like 1 protein	226	59

NM_013935	AAF05834.1	AF196571_1 Delta-like-1 protein	226	9.00e-59
	AAF21976.1	AF114494_1 putative tyrosine phosphatase	478 e-135	
	AAG10713.1	PTPLA	474 e-134	
	NP_055056.2	protein tyrosine phosphatase-like, member a; proline instead of catalytic arginine Similar to protein tyrosine phosphatase-like (proline instead of catalytic arginine),	472 e-133	
	AAH10353.1	member a	472 e-133	
NM_028784	XP_114343.2	similar to protein tyrosine phosphatase-like protein PTPLB [Mus musculus]	322	6.00e-88
	AAL12161.1	AF418272_1 coagulation factor XIII, A1 polypeptide A Chain A, Coagulation Factor XIII (A-Subunit Zymogen) (E.C.2.3.2.13)	482 e-135	
	1GGT	(Protein-Glutamine Gamma-Glutamyltransferase A Chain) B Chain B, Coagulation Factor XIII (A-Subunit Zymogen) (E.C.2.3.2.13)	482 e-135	
	1GGT	(Protein-Glutamine Gamma-Glutamyltransferase A Chain)	482 e-135	
	1F13	A Chain A, Recombinant Human Cellular Coagulation Factor XIII	482 e-135	
NP_083060.1	1F13	B Chain B, Recombinant Human Cellular Coagulation Factor XIII	482 e-135	
	1GGU	A Chain A, Human Factor XIII With Calcium Bound In The Ion Site	482 e-135	
	1GGY	A Chain A, Human Factor XIII With Ytterbium Bound In The Ion Site	482 e-135	
	1GGY	B Chain B, Human Factor XIII With Ytterbium Bound In The Ion Site	482 e-135	
	1QRK	A Chain A, Human Factor XIII With Strontium Bound In The Ion Site	482 e-135	
	1QRK	B Chain B, Human Factor XIII With Strontium Bound In The Ion Site	482 e-135	
	1GGU	B Chain B, Human Factor XIII With Calcium Bound In The Ion Site	482 e-135	
	CAC36886.1	bA525O21.1 (coagulation factor XIII, A1 polypeptide)	482 e-135	
	AAA52415.1	factor XIII a subunit coagulation factor XIII A1 subunit precursor; Coagulation factor XIII, A polypeptide;	481 e-135	
	NP_000120.1	TGase	481 e-135	
	AAA52488.1	clotting factor XIIIa precursor (EC 2.3.2.13)	481 e-135	

NM_009425 NP_033451.1	F:2.06	Mm.1062	F13A_HUMAN Coagulation factor XIII A chain precursor (Protein-glutamine		
			gamma-glutamyltransferase A chain) (Transglutaminase A chain)		481 e-135
			protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13), plasma		481 e-135
			A Chain A, Human Factor XIII With Calcium Bound In The Ion Site		481 e-135
			B Chain B, Human Factor XIII With Calcium Bound In The Ion Site		481 e-135
			factor XIII precursor		481 e-135
			A Chain A, Recombinant Human Coagulation Factor XIII		481 e-135
			B Chain B, Recombinant Human Coagulation Factor XIII		481 e-135
			coagulation factor XIII, A1 polypeptide		480 e-135
			tumor necrosis factor (ligand) superfamily, member 10; Apo-2 ligand; TNF-related		8.00e-
NP_003801.1	F:2.06	Mm.1062	apoptosis inducing ligand TRAIL		345 95
			TNF-related apoptosis inducing ligand TRAIL		8.00e-
			TNF10_HUMAN Tumor necrosis factor ligand superfamily member 10 (TNF-related		345 95
			apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L)		8.00e-
			TNF-related apoptosis inducing ligand TRAIL		345 95
			Apo-2 ligand		8.00e-
			tumor necrosis factor (ligand) superfamily, member 10		345 95
			A Chain A, Crystal Structure Of Apo2ITRAIL		4.00e-
			A Chain A, Crystal Structure Of Death Receptor 5 (Dr5) Bound To Apo2ITRAIL		2.00e-
			B Chain B, Crystal Structure Of Death Receptor 5 (Dr5) Bound To Apo2ITRAIL		2.00e-
NP_003801.1	F:2.06	Mm.1062	D Chain D, Crystal Structure Of Death Receptor 5 (Dr5) Bound To Apo2ITRAIL		2.00e-
			Apo-2 ligand		345 95
			tumor necrosis factor (ligand) superfamily, member 10		8.00e-
			A Chain A, Crystal Structure Of Apo2ITRAIL		4.00e-
			A Chain A, Crystal Structure Of Death Receptor 5 (Dr5) Bound To Apo2ITRAIL		2.00e-
			B Chain B, Crystal Structure Of Death Receptor 5 (Dr5) Bound To Apo2ITRAIL		2.00e-
			D Chain D, Crystal Structure Of Death Receptor 5 (Dr5) Bound To Apo2ITRAIL		2.00e-
			Apo-2 ligand		345 95
			tumor necrosis factor (ligand) superfamily, member 10		8.00e-
			A Chain A, Crystal Structure Of Apo2ITRAIL		4.00e-

[illegible]

AAA91639.1	lumican	291	2.00e-78
AAH07038.1	lumican	291	2.00e-78
AAH35997.1	lumican	291	2.00e-78
NP_002716.1	proline arginine-rich end leucine-rich repeat protein	235	2.00e-61
P51888	PRLP_HUMAN Prolargin precursor (Proline-arginine-rich end leucine-rich repeat protein)	235	2.00e-61
I39068	proline- arginine-rich end leucine-rich repeat protein PRELP precursor	235	2.00e-61
AAC50230.1	proline- arginine-rich end leucine-rich repeat protein	235	2.00e-61
AAC18782.1	prolargin	235	2.00e-61
AAH32498.1	proline arginine-rich end leucine-rich repeat protein	235	1.00e-61
NP_008966.1	keratocan; cornea plana 2 (autosomal recessive)	233	1.00e-60
O60938	KERA_HUMAN Keratocan precursor (KTN) (Keratan sulfate proteoglycan keratocan)	233	1.00e-60
AAC16390.1	keratan sulfate proteoglycan	233	1.00e-60
AAC17741.1	keratocan; kera; corneal keratan sulfate proteoglycan	233	1.00e-60
AAF69126.1	keratocan	233	1.00e-60

AAH32667.1	keratocan				233	60	1.00e-
NP_005005.1	osteoimodulin				207	53	8.00e-
Q99983	OMD_HUMAN Osteomodulin precursor (Osteoadherin) (OSAD) (Keratan sulfate proteoglycan osteomodulin) (KSPG osteomodulin)				207	53	8.00e-
BAA19055.1	osteoimodulin				207	53	8.00e-
BAA23982.1	Osteomodulin				207	53	8.00e-
AAH46356.1	osteoimodulin				207	53	8.00e-
AK002518							
BAC24996.1	Mm.27811	F:2.04			416	0	
NP_064575.1	HNOEL-iso protein				416	0	
AAF86881.1	AF201945_1 HNOEL-iso				416	0	
AAH09920.1	HNOEL-iso protein				416	0	
BAC11564.1	unnamed protein product				416	0	
BAC11644.1	unnamed protein product				416	0	
BAC11687.1	unnamed protein product				220	57	4.00e-
NM_013492	Mm.19634						
NP_038520.1	4	F:2.04			663	0	
NP_001822.1	complement cytolysis inhibitor precursor clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)				663	0	
P10909	CLUS_HUMAN Clusterin precursor (Complement-associated protein SP-40,40)				663	0	
A41386	(Complement cytolysis inhibitor) (CLI) (NA1/NA2) (Apolipoprotein J) (Apo-J) (TRPM-2) clusterin precursor				663	0	
CAA32847.1	SP-40,40 prepropeptide (AA -22 to 427)				663	0	

				TRPM-2 gene product			663	0
				apolipoprotein-J, Apo-J, SP-40,40=plasma glycoprotein/complement system				
				hemolysis modulator [human, seminal plasma, Peptide, 449 aa]			663	0
				TRPM-2 gene product			663	0
				clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2,				
				testosterone-repressed prostate message 2, apolipoprotein J)			663	0
				clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2,				
				testosterone-repressed prostate message 2, apolipoprotein J)			663	0
				apolipoprotein J precursor			632	0
				sulfated glycoprotein-2			590 e-168	
				'SP40,40'			481 e-136	
							9.00e-	
				CLU			202	52
NM_021607	Mm.21820							
NP_067620.1	3	F:2.04		KIAA0253			1247	0
				nicastatin			1247	0
				Nicastrin precursor			1247	0
				nicastatin			1247	0
				ATAG1874			1247	0
				NCSTN protein			1243	0
NM_009898	Mm.29043			coronin, actin binding protein, 1A; coronin, actin-binding, 1A;				
NP_034028.1	2	F:2.04		coronin, actin-binding protein, 1A; coronin-1			887	0
				Coronin-like protein p57 (Coronin 1A)			887	0
				actin-binding protein p57 - human			887	0
				human p57			887	0
				coronin homologue			887	0
				tryptophane aspartate-containing coat protein			887	0
				coronin-like protein			884	0
				coronin, actin binding protein, 1B			650	0

Q9BR76	Coronin 1B (Coronin 2)	650	0
AAH06449.1	Coronin, actin binding protein, 1B	650	0
T47172	hypothetical protein DKFZp762H186.1 - human (fragment)	638	0
CAB82406.1	hypothetical protein	638	0
	coronin, actin binding protein, 1C; coronin, actin-binding protein,		
NP_055140.1	1C; coronin 1C	638	0
Q9ULV4	Coronin 1C (Coronin 3) (hCRNN4)	638	0
BAA83077.1	hCRNN4	638	0
AAH02342.1	Coronin, actin binding protein, 1C	638	0
BAA76769.1	KIAA0925 protein	406	e-113
	coronin, actin binding protein, 2B; clipin C; coronin, actin-binding,		
NP_006082.1	2B; coronin, actin-binding protein, 2B	405	e-112
AAH26335.1	Coronin, actin binding protein, 2B	405	e-112
Q9UQ03	Coronin 2B (Coronin-like protein C) (ClipinC) (Protein FC96)	404	e-112
BAA36341.1	ClipinC	404	e-112
	coronin, actin binding protein, 2A; coronin, actin-binding protein,		
	2A; coronin 2A; coronin-like protein B; WD-repeat protein		
NP_438171.1	2; WD protein IR10	395	e-109
Q92828	Coronin 2A (WD-repeat protein 2) (IR10)	395	e-109
AAH00010.1	Coronin, actin binding protein, 2A	395	e-109
AAH11690.1	Coronin, actin binding protein, 2A	395	e-109
	coronin, actin binding protein, 2A; coronin, actin-binding protein,		
	2A; coronin 2A; coronin-like protein B; WD-repeat protein		
NP_003380.2	2; WD protein IR10	394	e-109
	endothelial differentiation, sphingolipid G-protein-coupled receptor,		
	1; edg-1; G protein-coupled sphingolipid receptor;		
NM_007901			
O08530			
		683	0
		683	0
		683	0

P21453	Probable G protein-coupled receptor EDG-1	674	0
A35300	G protein-coupled receptor edg-1 - human	674	0
AAA52336.1	endothelial differentiation protein (edg-1)	674	0
AAC51905.1	G protein-coupled receptor	674	0
AAK01993.1	EDG1	596	e-170
	endothelial differentiation, sphingolipid G-protein-coupled receptor, 3; G protein-coupled receptor, endothelial differentiation gene-3; S1P receptor EDG3; sphingosine 1-phosphate receptor 3; chromosome 9 open reading frame 47	369	e-101
NP_005217.2		369	e-101
AAP84353.1	endothelial differentiation sphingolipid G-protein-coupled receptor 3		
	Endothelial differentiation, sphingolipid G-protein-coupled receptor, 3	369	e-101
AAH60827.1	Sphingosine 1-phosphate receptor Edg-3 (S1P receptor Edg-3) (Endothelial differentiation G-protein-coupled receptor 3)	368	e-101
Q99500	G protein-coupled receptor - human	368	e-101
JC5245	G-protein coupled receptor (putative)	368	e-101
CAA58744.1	lysosphingolipid receptor	368	e-101
AAC51906.1	endothelial differentiation, sphingolipid G-protein-coupled receptor, 8; sphingosine 1-phosphate receptor Edg-8; sphingosine 1-phosphate receptor 5	317	1e-085
NP_110387.1		317	1e-085
AAG38113.1	sphingosine 1-phosphate receptor Edg-8	317	1e-085
AAL57041.1	SPPR	317	1e-085
BAB89315.1	putative G-protein coupled receptor	317	1e-085
	Endothelial differentiation, sphingolipid G-protein-coupled receptor, 8	317	1e-085
AAH34703.1		317	1e-085
BAC11119.1	unnamed protein product	317	1e-085

AAP20653.1	G-protein coupled receptor EDG8 Sphingosine 1-phosphate receptor Edg-5 (S1P receptor Edg-5) (Endothelial differentiation G-protein coupled receptor 5)	317 1e-085
O95136		313 1e-084
AAP20652.1	G-protein coupled receptor EDG5 endothelial differentiation, sphingolipid G-protein-coupled receptor, 5; S1P receptor EDG5; sphingosine 1-phosphate receptor 2 lysosphingolipid receptor Edg5 endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2; ventricular zone gene-1	313 1e-084
NP_004221.1		310 9e-084
AAC98919.1		310 9e-084
NP_001392.2		236 1e-061
NP_476500.1		236 1e-061
Q92633	Lysophosphatidic acid receptor Edg-2 (LPA receptor 1) (LPA-1) G protein-coupled receptor Edg-2	236 1e-061
CAA70686.1		236 1e-061
AAC00530.1	Edg-2 receptor	236 1e-061
AAH30615.1	EDG2 protein Endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	236 1e-061
AAH36034.1		236 1e-061
AAP84359.1	endothelial differentiation G-protein-coupled receptor 2	236 1e-061
JC5293	lysophosphatidic acid receptor - human	236 1e-061
AAC51139.1	lysophosphatidic acid receptor homolog	236 1e-061
NM_019578		
NP_062524.1	exostoses (multiple)-like 1 Exostosin-like 1 (Glucuronosyl-N-acetylglucosaminyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase) (Exostosin-L) (Multiple exostosin-like protein) multiple exostosin-like protein	975 0
Q92935		975 0
AAC51141.1		975 0

AAD02840.1	multiple exostoses-like 1	975	0
AAF73172.1	exostoses-like protein 1	975	0
	Exostosin-1 (Glucuronosyl-N-acetylglucosaminyl-proteoglycan/N-acetylglucosaminyl-proteoglycan		
Q16394	4-alpha-N-acetylglucosaminyltransferase) (Putative tumor suppressor protein EXT1) (Multiple exostoses protein 1)	530	0
AAH01174.1	Exostoses (multiple) 1	530	0
NP_000118.1	exostoses (multiple) 1	526	e-149
	putative tumour suppressor/hereditary multiple exostoses candidate		
AAB62283.1	gene	526	e-149
2204384A	EXT1 gene	526	e-149
NP_000392.1	exostoses (multiple) 2	271	5e-072
	Exostosin-2 (Glucuronosyl-N-acetylglucosaminyl-proteoglycan/N-acetylglucosaminyl-proteoglycan		
	4-alpha-N-acetylglucosaminyltransferase) (Putative tumor suppressor protein EXT2) (Multiple exostoses protein 2)	271	5e-072
Q93063	EXT2	271	5e-072
AAB07008.1	multiple exostosis 2	271	5e-072
AAC51219.1	hereditary multiple exostoses gene 2 protein	271	5e-072
AAC50764.1	EXT2 protein	271	5e-072
AAH10058.1	multiple exostoses type II protein EXT2.I	247	1e-064
AAB62718.1	a disintegrin and metalloprotease with thrombospondin motifs-2 isoform 1; procollagen	8.00e-	
AA832579	I N-proteinase; Procollagen N-endorpeptidase	240	64
XP_109830.2	NP_055059.1		
	ATS2_HUMAN ADAMTS-2 precursor (A disintegrin and metalloproteinase with thrombospondin motifs 2) (ADAM-TS 2) (ADAM-TS2) Procollagen I/II		
	amino-propeptide processing enzyme) (Procollagen I N-proteinase) (PC I-NP) (Procollagen N-endorpeptidase) (pNPI)	8.00e-	
O95450		240	64

				CAA05880.1	procollagen I N-proteinase			240	64	8.00e-
				AAH16451.1	AAH16451 Unknown (protein for IMAGE:3451933)			160	50	2.00e-
NM_008760				NP_054776.1	osteoinductin preproprotein; osteoinductive factor; mimecan			495	e-140	
NP_032786.1	F:2.03	Mm.4258		NP_077727.1	osteoinductin preproprotein; osteoinductive factor; mimecan			495	e-140	
				NP_148935.1	osteoinductin preproprotein; osteoinductive factor; mimecan			495	e-140	
				P20774	MIME_HUMAN Mimecan precursor (Osteoglycin) (Osteoinductive factor) (OIF)			495	e-140	
				B35272	osteoinductive factor			495	e-140	
				AAD43022.1	osteoinductive factor OIF			495	e-140	
				CAB53706.1	hypothetical protein			495	e-140	
				AAF19364.1	mimecan			495	e-140	
				AAF69109.1	AF202167_1 mimecan			495	e-140	
				AAH37273.1	osteoinductin (osteoinductive factor, mimecan)			495	e-140	
								2.00e-		
				CAB61417.1	hypothetical protein			241	63	
					PGLB_HUMAN Dermatan sulfate proteoglycan 3 precursor (Epiphygan) (Small			1.00e-		
				Q99645	chondroitin/dermatan sulfate proteoglycan) (Proteoglycan-Lb) (PG-Lb)			215	55	
								1.00e-		
				AAH30958.1	dermatan sulfate proteoglycan 3			215	55	
								3.00e-		
				NP_004941.1	dermatan sulfate proteoglycan 3; Pg-Lb; dermatan sulphate proteoglycan 3			210	54	
								3.00e-		
				AAC50945.1	dermatan sulfate proteoglycan 3			210	54	
								3.00e-		
				NP_055174.1	opticin; oculoglycan; opticin, oculoglycan			204	52	
								3.00e-		
				Q9UBM4	OPT_HUMAN Opticin precursor (Oculoglycan)			204	52	

Accession	Gene	Protein	Length	Score
AAD45900.1	AF161702_1	oculoglycan	204	3.00e-52
CAB53459.1	opticin	opticin	204	3.00e-52
AAL78286.1	opticin	cartilage oligomeric matrix protein precursor; epiphyseal dysplasia, multiple 1; pseudoachondroplasia (epiphyseal dysplasia 1, multiple); cartilage oligomeric matrix protein(pseudoachondroplasia, epiphyseal dysplasia 1, multiple)	1245	0
NP_000086.1	F:2.03	COMP_HUMAN Cartilage oligomeric matrix protein precursor (COMP)	1245	0
P49747		matrix protein	1245	0
AAA57253.1		cartilage oligomeric matrix protein	1245	0
BAC53888.1		COMP_HUMAN	1234	0
AAB86501.1		Similar to cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple)	1217	0
AAH33676.1		thrombospondin 4	927	0
NP_003239.1		TSP4_HUMAN Thrombospondin 4 precursor	927	0
P35443		thrombospondin 4 precursor	927	0
TSHUP4		thrombospondin-4	858	0
CAA79635.1		thrombospondin 3	858	0
NP_009043.1		TSP3_HUMAN Thrombospondin 3 precursor	858	0
P49746		thrombospondin 3 precursor	858	0
A57121		thrombospondin 3	716	0
AAC41762.1		Similar to thrombospondin 1	567	e-161
AAH18786.1		precursor polypeptide (AA -31 to 1139)	567	e-161
NP_003237.1		TSP1_HUMAN Thrombospondin 1 precursor	567	e-161
CAA32889.1		thrombospondin 1 precursor	567	e-161
P07996		precursor polypeptide (AA -18 to 1152)	567	e-161
TSHUP1			567	e-161
CAA28370.1			567	e-161

				1304281A	thrombospondin	567 e-161
				NP_003238.1	thrombospondin 2	550 e-156
				P35442	TSP2_HUMAN Thrombospondin 2 precursor	550 e-156
				TSHUP2	thrombospondin 2 precursor	550 e-156
				AAA03703.1	thrombospondin 2	550 e-156
				AAC51818.1	thrombospondin3	467 e-131
NM_009762	Mm.23427				SET and MYND domain containing 1; CD8 beta opposite; zinc finger,	
NP_033892.1	4	F-2.03		NP_938015.1	MYND domain containing 18	935 0
				Q8NB12	SET and MYND domain containing protein 1	935 0
				BAC03732.1	unnamed protein product	935 0
					SET and MYND domain containing 2; HSKM-B protein; zinc finger, MYND	
				NP_064582.1	domain containing 14	243 7e-064
				AAF86953.1	HSKM-B	243 7e-064
				Q9H7B4	SET and MYND domain containing protein 3 (Zinc finger MYND domain containing protein 1)	233 9e-061
				AAH31010.1	SMYD3 protein	233 9e-061
				AAH49367.1	SMYD2 protein	224 4e-058
					SET and MYND domain containing 3; zinc finger protein, subfamily 3A	
					(MYND domain containing), 1; zinc finger, MYND domain	
				NP_073580.1	containing 1	210 6e-054
				BAB14981.1	unnamed protein product	210 6e-054
					transducin-like enhancer protein 4; transducin-like enhancer of split	
U61363	Mm.10363				4; enhancer of split groucho 4; B lymphocyte gene 1	1043 0
S35681	8	F-2.03		NP_008936.2	Transducin-like enhancer protein 4	1043 0
				Q04727	hypothetical protein DKFZp547P103.1 - human (fragment)	1043 0
				T47149	hypothetical protein	1043 0
				CAB82397.1	hypothetical protein	1043 0
				BAA86575.1	KIAA1261 protein	1043 0
				AAH59405.1	TLE4 protein	1026 0

NM_010610	NP_005068.2	transducin-like enhancer protein 1; enhancer of split groucho 1;	0
	Q04724	transducin-like enhancer of split 1	947
	AAH10100.1	Transducin-like enhancer protein 1 (ESG1)	947
	AAH15747.1	Transducin-like enhancer protein 1	947
	B56695	Transducin-like enhancer protein 1	947
	AAA61192.1	transducin-like enhancer-of-split homolog TLE-1 - human	941
	AAA61195.1	transducin-like enhancer protein	941
	AAH41831.1	transducin-like enhancer protein	912
	AAH43247.1	TLE3 protein	889
	AAH43247.1	TLE3 protein	889
NP_034740.1	BAD06365.1	stretch-activated Kca channel	2187
	S62904	calcium-regulated potassium channel alpha chain - human	1973
	AAB65837.1	large conductance calcium- and voltage-dependent potassium channel	0
	2209275A	alpha subunit	1973
	AAA85104.1	maxi K channel:SUBUNIT=alpha	1973
		large-conductance calcium-activated potassium channel	0
		large conductance calcium-activated potassium channel subfamily M	0
		alpha member 1; Drosophila slowpoke-like;	0
	NP_002238.2	stretch-activated Kca channel; BKCA alpha subunit	1973
	AAA92290.1	calcium-activated potassium channel	1973
	2121221A	Ca-activated K channel	1973
	AAB88802.1	calcium-activated potassium channel alpha subunit	1973
		large conductance calcium-activated potassium channel subfamily M	0
	AAK91504.1	alpha member 1	1973
	AAC50353.1	calcium activated potassium channel	1971
	AAD31173.1	BKCA alpha subunit; MaxiK alpha subunit; Slo alpha subunit	1969
	BAD06397.1	BK variant stretch-activated Kca channel	1953
	AAA50173.1	calcium-activated potassium channel	1593
			0
			0

NM_009673	I38596			calcium-activated potassium channel - human (fragment)	1155	0
	AAA50216.1			calcium-activated potassium channel	1155	0
NP_033803.1	1HVD	F:2.02	Mm.1620	Annexin V (Lipocortin V, Endonexin II, Placental Anticoagulant Protein) (Calcium Ions Are Visible) Mutation With Glu 17 Replaced By Gly (E17g)	566	e-161
				Annexin V (Lipocortin V, Endonexin II, Placental Anticoagulant Protein) Mutant With Glu 17 Replaced By Gly, Glu 78 Replaced By Gln (E17g,E78g) Complexed With Calcium	565	e-161
	1HVF			A Chain A, Annexin V	563	e-160
	1ANW			B Chain B, Annexin V	563	e-160
	1ANW			A Chain A, Annexin V	563	e-160
	1ANX			B Chain B, Annexin V	563	e-160
	1ANX			C Chain C, Annexin V	563	e-160
	NP_001145.1			annexin V; endonexin II; anchorin CII; lipocortin V; placental anticoagulant protein I ANX5_HUMAN Annexin V (Lipocortin V) (Endonexin II) (Calphobindin I) (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha) (Anchorin CII)	563	e-160
	P08758			annexin V	563	e-160
	AQHUP			A Chain A, Annexin V (Hexagonal Crystal Form)	563	e-160
	1AVH			B Chain B, Annexin V (Hexagonal Crystal Form)	563	e-160
	1AVH			Annexin V (Rhomboidal Crystal Form)	563	e-160
	1AVR			B Chain B, Crystal Structure Of Recombinant Human Placental Annexin V Complexed With K-201 As A Calcium Channel Activity Inhibitor	563	e-160
	1HAK			A Chain A, Crystal Structure Of Recombinant Human Placental Annexin V Complexed With K-201 As A Calcium Channel Activity Inhibitor	563	e-160
	CAA30985.1			VAC protein (AA 1-320)	563	e-160
	AAA35570.1			anticoagulant precursor (5' end put.); putative	563	e-160
	AAA52386.1			endonexin II	563	e-160
	AAB59545.1			anticoagulant protein 4	563	e-160
	BAA00122.1			blood coagulation inhibitor	563	e-160

AAA36166.1	lipocortin-V	563 e-160
AAB40047.1	annexin V	563 e-160
AAB60648.1	annexin V	563 e-160
AAH01429.1	annexin A5	563 e-160
AAH04993.1	annexin A5	563 e-160
AAH12804.1	Similar to annexin A5	563 e-160
AAH12822.1	Similar to annexin A5	563 e-160
1512315A	calphobindin	563 e-160
1313303A	coagulation inhibitor	563 e-160
1HVE	Annexin V (Lipocortin V, Endonexin II, Placental Anticoagulant Protein) (Calcium Ions Are Visible) Mutant With Glu 78 Replaced By Gln (E78q)	562 e-160
1HVG	Annexin V (Lipocortin V, Endonexin II, Placental Anticoagulant Protein) (Calcium Ions Are Visible) Mutant With Glu 78 Replaced By Gln (E78q) (Second Crystal Form)	562 e-160
AAH18671.1	annexin A5	561 e-160
1SAV	Human Annexin V With Proline Substitution By Thioproline	546 e-155
1M9I	A Chain A, Crystal Structure Of Phosphorylation-Mimicking Mutant T356d Of Annexin VI	2.00e-96
CAA68286.1	protein p68 (1 - 673)	351 96
P08133	ANX6_HUMAN Annexin VI (Lipocortin VI) (P68) (P70) (Protein III) (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II)	2.00e-96
AQHU68	annexin VI	351 96
BAA00400.1	calphobindin II	2.00e-96
AAH17046.1	annexin A6	351 96
1510256A	calphobindin II	2.00e-96

NM_011638	NP_035768.1	Mm.26069	F:2.02	NP_003225.1	transferrin receptor (p90, CD71); Transferrin receptor	1196	0
					TFR1_HUMAN Transferrin receptor protein 1 (TFR1) (TR) (TFR) (Tfr) (CD71 antigen)		
	P02786				(T9) (p90)	1196	0
	JXHU				transferrin receptor	1196	0
	CAA25527.1				put. transferrin receptor (aa 1-760)	1196	0
	AAA61153.1				transferrin receptor	1196	0
	1011297A				transferrin receptor	1196	0
	AAF04564.1				AF187320_1 transferrin receptor	1195	0
	AAH01188.1				transferrin receptor (p90, CD71)	1195	0
	1DE4				C Chain C, Hemochromatosis Protein Hfe Complexed With Transferrin Receptor	1023	0
	1DE4				F Chain F, Hemochromatosis Protein Hfe Complexed With Transferrin Receptor	1023	0
	1DE4				I Chain I, Hemochromatosis Protein Hfe Complexed With Transferrin Receptor	1023	0
	1CX8				A Chain A, Crytal Structure Of The Ectodomain Of Human Transferrin Receptor	1020	0
	1CX8				B Chain B, Crytal Structure Of The Ectodomain Of Human Transferrin Receptor	1020	0
	1CX8				C Chain C, Crytal Structure Of The Ectodomain Of Human Transferrin Receptor	1020	0
	1CX8				D Chain D, Crytal Structure Of The Ectodomain Of Human Transferrin Receptor	1020	0
	1CX8				E Chain E, Crytal Structure Of The Ectodomain Of Human Transferrin Receptor	1020	0
	1CX8				F Chain F, Crytal Structure Of The Ectodomain Of Human Transferrin Receptor	1020	0
	1CX8				G Chain G, Crytal Structure Of The Ectodomain Of Human Transferrin Receptor	1020	0
	1CX8				H Chain H, Crytal Structure Of The Ectodomain Of Human Transferrin Receptor	1020	0
	Q9UP52				TFR2_HUMAN Transferrin receptor protein 2 (TFR2)	545 e-154	
	AAD45561.1				AF067864_1 transferrin receptor 2 alpha	545 e-154	
	NP_003218.1				transferrin receptor 2	498 e-140	
	AAC78796.1				transferrin-receptor2	498 e-140	
						2.00e-	
	BAA91153.1				unnamed protein product	315	85
	AAC83972.1				prostate-specific membrane antigen	228	59

NP_004467.1	folate hydrolase (prostate-specific membrane antigen) 1; folate hydrolase 1 (prostate-specific membrane antigen)	228	3.00e-59
Q04609	FOH1_HUMAN Glutamate carboxypeptidase II (Membrane glutamate carboxypeptidase) (mGCP) (N-acetylated-alpha-linked acidic dipeptidase I) (NAALADase I) (Pteroylpoly-gamma-glutamate carboxypeptidase) (Folypoly-gamma-glutamate carboxypeptidase) (FGCP) (Folate hydrolase 1) (Prostate-specific membrane antigen) (PSMA) (PSM)	228	3.00e-59
A56881	prostate-specific membrane antigen	228	3.00e-59
AAA60209.1	prostate-specific membrane antigen	228	3.00e-59
AAD51121.1	AF176574_1 folypoly-gamma-glutamate carboxypeptidase	228	3.00e-59
AAM34479.1	prostate-specific membrane antigen	228	3.00e-59
NP_005458.1	N-acetylated alpha-linked acidic dipeptidase 2; N-acetylated alpha-linked acidic dipeptidase II	216	1.00e-55
Q9Y3Q0	NLD2_HUMAN N-acetylated-alpha-linked acidic dipeptidase II (NAALADase II)	216	1.00e-55
CAB39967.1	NAALADase II protein	216	1.00e-55
NP_057491.1	chromosome 20 open reading frame 43	393	e-109
AAF29128.1	HSPC164	393	e-109
Q9BY42	Protein C20orf43 (HSPC164/HSPC169) (AD-007) (CDA05)	393	e-109
AAF29133.1	HSPC169	393	e-109
AAH03359.1	C20orf43 protein	393	e-109
CAC03740.1	dJ1153D9.1.1 (novel protein)	392	e-109

AK009901

BAB26573.1

Mm.25157 F:2.02

U57327	Mm.29519	BAA91193.1	unnamed protein product	390 e-108
P70323	4	AAF17212.1	protein x 0001	389 e-108
		AAK14929.1	CDA05	389 e-108
			T-box 1 isoform A; brachyury; T-box 1 transcription factor C;	
	F:2.02	NP_542377.1	Testis-specific T-box protein	350 6e-097
			T-box transcription factor TBX1 (T-box protein 1) (Testis-specific	
		O43435	T-box protein)	350 6e-097
		AAB94018.1	brachyury	350 6e-097
			T-box 1 isoform C; brachyury; T-box 1 transcription factor C;	
		NP_542378.1	Testis-specific T-box protein	350 6e-097
		AAK58955.1	T-box 1 transcription factor C	350 6e-097
			T-box 1 isoform B; brachyury; T-box 1 transcription factor C;	
		NP_005983.1	Testis-specific T-box protein	350 6e-097
		AAB94019.1	brachyury	350 6e-097
		NP_005986.2	T-box 10	310 1e-084
		AAO73483.1	transcription factor TBX10	310 1e-084
		NP_065150.1	T-box transcription factor TBX20; T-box protein 20	224 5e-059
		CAB51916.1	T-box transcription factor	224 5e-059
		Q9UMR3	T-box transcription factor TBX20 (T-box protein 20)	224 5e-059
		AAD21787.1	similar to fly T-box protein H15; similar to Q94890 (PID:g2501131)	224 5e-059
		O75333	T-box transcription factor TBX10 (T-box protein 10)	213 2e-055
		AAC23481.1	T-box-containing transcriptional activator	213 2e-055
		NP_060958.2	T-box 4	210 1e-054
		P57082	T-box transcription factor TBX4 (T-box protein 4)	210 1e-054
			ras homolog gene family, member C; Aplysia RAS-related homolog 9	
NM_007484			(oncogene RHO H9); Aplysia ras-related homolog 9; RhoC;	
Q62159	Mm.262	NP_786886.1	RAS homolog gene family, member C (oncogene RHO H9)	394 e-109
		P08134	Transforming protein RhoC (H9)	394 e-109
		TVHURC	GTP-binding protein rhoC - human	394 e-109

CAA29969.1	unnamed protein product	394	e-109
AAC33179.1	GTPase I	394	e-109
AAH07245.1	Ras homolog gene family, member C	394	e-109
AAH09177.1	Ras homolog gene family, member C	394	e-109
AAM21119.1	small GTP binding protein RhoC	394	e-109
AAH52808.1	Ras homolog gene family, member C	394	e-109
NP_001655.1	oncogene RHO H12	369	e-102
P06749	Transforming protein RhoA (H12)	369	e-102
TVHU12	GTP-binding protein rhoA - human	369	e-102
CAA28690.1	unnamed protein product	369	e-102
AAC33178.1	GTP-binding protein	369	e-102
AAH01360.1	ARHA protein	369	e-102
AAH05976.1	ARHA protein	369	e-102
AAM21117.1	small GTP binding protein RhoA	369	e-102
CAE46190.1	hypothetical protein	369	e-102
1LB1 B	Chain B, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs In Complex With RhoA	365	e-101
1LB1 D	Chain D, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs In Complex With RhoA	365	e-101
1LB1 F	Chain F, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs In Complex With RhoA	365	e-101
1LB1 H	Chain H, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs In Complex With RhoA	365	e-101
1FTN	Crystal Structure Of The Human RhoGDP COMPLEX	365	e-101
1OW3 B	Chain B, Crystal Structure Of RhoA.Gdp.Mgf3-In Complex With Rhogap	365	e-101
1CC0 A	Chain A, Crystal Structure Of The RhoA.Gdp-Rhogdi Complex	363	e-100
1CC0 C	Chain C, Crystal Structure Of The RhoA.Gdp-Rhogdi Complex	363	e-100
AAA50612.1	multidrug resistance protein	362	e-100

NM_008524 NP_032550.1	1A2B	Human RhoA Complexed With Gtp Analogue	352 4e-097
	1CXZ A	Chain A, Crystal Structure Of Human RhoA Complexed With The Effector Domain Of The Protein Kinase PknPRK1	352 4e-097
	1KMQ A	Chain A, Crystal Structure Of A Constitutively Activated RhoA Mutant (Q63I)	344 1e-094
	1DPF A	Chain A, Crystal Structure Of A Mg-Free Form Of RhoA Complexed With Gdp	343 3e-094
	1TX4 B	Chain B, RhoRHOGAPGDP(DOT)ALF4 COMPLEX	335 7e-092
	F:2.01	NP_002336.1 lumican	574 e-163
	P51884	LUM_HUMAN Lumican precursor (Keratan sulfate proteoglycan lumican) (KSPG lumican)	574 e-163
	AAA91639.1	lumican	574 e-163
	AAH07038.1	lumican	574 e-163
	AAH35997.1	lumican	574 e-163
	AAA85268.1	lumican	570 e-162
	AAH35281.1	Similar to fibromodulin	1.00e-78
	Q06828	FMOD_HUMAN Fibromodulin precursor (FM) (Collagen-binding 59 kDa protein) (Keratan sulfate proteoglycan fibromodulin) (KSPG fibromodulin)	2.00e-77
	CAA51418.1	fibromodulin	2.00e-77
	NP_002014.1	fibromodulin precursor	1.00e-76
	S55275	fibromodulin precursor	1.00e-76
	CAA53233.1	fibromodulin	1.00e-76
			285 76
			285 76
			285 76

NP_008966.1	keratocan; cornea plana 2 (autosomal recessive)	220	57	4.00e-
O60938	KERA_HUMAN Keratocan precursor (KTN) (Keratan sulfate proteoglycan keratocan)	220	57	4.00e-
AAC16390.1	keratan sulfate proteoglycan	220	57	4.00e-
AAC17741.1	keratocan; kera; corneal keratan sulfate proteoglycan	220	57	4.00e-
AAF69126.1	keratocan	220	57	4.00e-
AAH32667.1	keratocan	220	57	2.00e-
NP_002716.1	proline arginine-rich end leucine-rich repeat protein	218	56	2.00e-
P51888	PRLP_HUMAN Prolargin precursor (Proline-arginine-rich end leucine-rich repeat protein)	218	56	2.00e-
I39068	proline- arginine-rich end leucine-rich repeat protein PRELP precursor	218	56	2.00e-
AAC50230.1	proline- arginine-rich end leucine-rich repeat protein	218	56	2.00e-
AAC18782.1	prolargin	218	56	2.00e-
AAH32498.1	proline arginine-rich end leucine-rich repeat protein	218	56	3.00e-
NP_005005.1	osteonodulin	211	54	3.00e-
Q99983	OMD_HUMAN Osteomodulin precursor (Osteoadherin) (OSAD) (Keratan sulfate proteoglycan osteomodulin) (KSPG osteomodulin)	211	54	3.00e-

NM_008594 A55182	Mm.2759	F:2.01	1	BAA19055.1	osteomodulin	211	3.00e-54
				BAA23982.1	Osteomodulin	211	3.00e-54
				AAH46356.1	osteomodulin	211	3.00e-54
				NP_005919.	milk fat globule-EGF factor 8 protein; lactadherin; medin; O-acetyl		
				1	disialoganglioside synthase	427	e-119
					MFGM_HUMAN Lactadherin precursor (Milk fat globule-EGF factor 8)		
				Q08431	(MFG-E8) (HMFG) (Breast epithelial antigen BA46) (MFGM)	427	e-119
				AAC50549.1	BA46	427	e-119
				AAN08508.			
				1.	epididymal protein	427	e-119
				2211263A	breast epithelial BA46 antigen	427	e-119
				AAH53656.1	EDIL3 protein	415	e-115
				AAH30828.1	EGF-like repeats and discoidin I-like domains-containing protein 3	412	e-114
				NP_005702.	EGF-like repeats and discoidin I-like domains-containing protein 3;		
				3	developmental endothelial locus-1	412	e-114
					EDI3_HUMAN EGF-like repeats and discoidin I-like domains protein 3		
					precursor (Developmentally regulated endothelial cell locus 1 protein)		
				Q43854	(Integrin-binding protein DEL1)	412	e-114
				AAC02648.1	integrin binding protein Del-1	412	e-114
				CAD97938.1	hypothetical protein	383	e-106
				AAH03610.1	MFGES protein	339	9e-093
				AAP35594.1	milk fat globule-EGF factor 8 protein	339	9e-093
				A47285	milk fat globule protein	268	2e-071

	AB19771.1	HMFG			268 2e-071
	AAA52420.1	coagulation factor VIII			224 3e-058
	1012298A	factor VIIIC			224 3e-058
	CAA25619.1	unnamed protein product			224 3e-058
NM_008733					
NP_032759.1	Mm.6384	F:2.01	NP_932326.1	ebulin-related anchoring protein isoform S	3024 0.0
			AAO47073.1	nebulin-related anchoring protein isoform S	3024 0.0
			CAD89899.1	hypothetical protein	3020 0.0
			CAE46027.1	hypothetical protein	3020 0.0
			CAD38623.1	ypothetical protein	3018 0.0
			CAE45811.1	hypothetical protein	3016 0.0
			CAE45846.1	hypothetical protein	3012 0.0
			CAD89910.1	hypothetical protein	3008 0.0
			AAO47074.1	nebulin-related anchoring protein isoform C	2882 0.0
			NP_006166.2	nebulin-related anchoring protein isoform C	2881 0.0
			AAL99185.2	nebulin-related anchoring protein	2881 0.0
			CAD89998.1	hypothetical protein	2215 0.0
AAH17439.					
AK005364					
BAC25113.1	Mm.94560	F:2.01	1	Unknown (protein for MGC:12958)	303 5e-082
			BAC77358.1	putative NFkB activating protein	303 5e-082
			BAC77385.1	putative MAPK activating protein	303 5e-082
			AAH02490.		
			2	Unknown (protein for MGC:915)	303 5e-082
			AAF36115.1	HSPC195	265 1e-070
			NP_057547.		
			4	hypothetical protein HSPC195	262 1e-069

BAA91907.1	unnamed protein product	262 1e-069
AAG01986.	similar to Homo sapiens hypothetical protein (HSPC195)mRNA with GenBank	
1	Accession Number AF151029	262 1e-069
AAH06428.		
1	Hypothetical protein HSPC195	262 1e-069
NM_008125		
NP_032151.1	Mm.34118 F:2	
AAF91440.1	AF281280_1 gap junction protein beta 2	450 e-127
CAC16959.1	bA264J4.5 (gap junction protein beta 2, 26 kD (connexin 26))	450 e-127
AAH17048.1	Unknown (protein for MGC:9238)	450 e-127
AAL87696.1	AF479776_1 connexin 26	450 e-127
	gap junction protein, beta 2, 26kDa (connexin 26); gap junction protein, beta 2, 26kD	
NP_003995.1	(connexin 26)	449 e-126
P29033	CXB2_HUMAN Gap junction beta-2 protein (Connexin 26) (Cx26)	449 e-126
A43424	gap junction protein Cx26	449 e-126
AAD21314.1	connexin 26	449 e-126
AAH38934.1	gap junction protein, beta 6 (connexin 30)	379 e-105
NP_006774.1	gap junction protein, beta 6 (connexin 30)	377 e-104
O95452	CXB6_HUMAN Gap junction beta-6 protein (Connexin 30) (Cx30)	377 e-104
CAA06611.1	unnamed protein product	377 e-104
	gap junction protein, beta 1, 32kDa (connexin 32, Charcot-Marie-Tooth neuropathy, X-linked); Gap junction protein, beta-1, 32kD (connexin 32); gap junction protein, beta	
NP_000157.1	1, 32kD (connexin 32, Charcot-Marie-Tooth neuropathy, X-linked)	2.00e- 319 87
P08034	CXB1_HUMAN Gap junction beta-1 protein (Connexin 32) (Cx32) (GAP junction 28 kDa liver protein)	2.00e- 319 87
B29005	gap junction protein Cx32	2.00e- 319 87
CAA27856.1	gap junction protein (aa 1-283)	2.00e- 319 87

AAH02805.1	gap junction protein, beta 1, 32kD (connexin 32)	319	2.00e-87
	gap junction protein, beta 1, 32kD (connexin 32, Charcot-Marie-Tooth neuropathy, X-linked)	319	2.00e-87
AAH22426.1	gap junction protein, beta 1, 32kDa (connexin 32, Charcot-Marie-Tooth neuropathy, X-linked)	319	2.00e-87
AAH39198.1	gap junction protein, beta 3, 31kDa (connexin 31); gap junction protein, beta 3, 31kD (connexin 31)	256	1.00e-68
NP_076872.1		256	1.00e-68
O75712	CXB3_HUMAN Gap junction beta-3 protein (Connexin 31) (Cx31)	256	1.00e-68
JE0274	connexin 31	256	1.00e-68
CAA06165.1	connexin31	256	1.00e-68
AAD11816.1	connexin 31; gap junctional protein cx31	256	1.00e-68
AAC95471.1	connexin 31	256	1.00e-68
CAB90269.1	dJ34M23.2 (gap junction protein, beta 3, 31kD (connexin 31))	256	1.00e-68
AAH12918.1	gap junction protein, beta 3, 31kD (connexin 31)	256	1.00e-68
NP_694944.1	gap junction protein, beta 4; connexin 30.3	254	5.00e-68
Q9NTQ9	CXB4_HUMAN Gap junction beta-4 protein (Connexin 30.3) (Cx30.3)	254	5.00e-68
CAB90270.1	dJ34M23.3 (gap junction protein, beta 4 (connexin 30.3))	254	5.00e-68

AAH34709.1	similar to Gap junction beta-4 protein (Connexin 30.3) (Cx30.3)	254	5.00e-68
NP_005259.1	gap junction protein, beta 5 (connexin 31.1)	241	5.00e-64
O95377	CXB5_HUMAN Gap junction beta-5 protein (Connexin 31.1) (Cx31.1)	241	5.00e-64
AAD18005.1	connexin 31.1; gap junctional protein cx31.1	241	5.00e-64
CAB90271.1	dJ34M23.4 (gap junction protein, beta 5 (connexin 31.1))	241	5.00e-64
AAH04379.1	gap junction protein, beta 5 (connexin 31.1)	241	5.00e-64
AAC95472.1	connexin 31.1 gap junction protein, alpha 8, 50kDa (connexin 50); gap junction membrane channel protein alpha-8	241	8.00e-64
NP_005258.1	(connexin 50); gap junction protein, alpha 8, 50kD (connexin 50)	241	8.00e-64
I39176	intrinsic membrane protein MP70	241	8.00e-64
AAA77062.1	gap junction membrane channel protein alpha-8	241	8.00e-64
AAA96152.1	insulin-like growth factor-I	248	6.00e-66
P05019	IGFB_HUMAN Insulin-like growth factor IB precursor (IGF-IB) (Somatomedin C)	237	8.00e-63
IGHU1B	insulin-like growth factor I precursor, splice form B	237	8.00e-63

NM_010512

NP_034642.1

Mm.2770

F:2

CAA40093.1	IGF-1b	237	8.00e-63
AAA52537.1	insulin-like growth factor IB	237	8.00e-63
AAA52539.1	insulin-like growth factor IB prepropeptide	237	8.00e-63
A36552	insulin-like growth factor 1a precursor	227	9.00e-60
AAA52789.1	insulin-like growth factor I	227	9.00e-60
1001199A	insulin-like growth factor I precursor	223	2.00e-58
NP_000609.1	insulin-like growth factor 1 (somatomedin C); insulin-like growth factor 1 (somatomedia C)	223	2.00e-58
P01343	IGFA_HUMAN Insulin-like growth factor IA precursor (IGF-IA) (Somatomedin C)	223	2.00e-58
IGHU1	insulin-like growth factor I precursor, splice form A	223	2.00e-58
CAA40092.1	IGF-1a	223	2.00e-58
CAA40342.1	insulin-like growth factor I	223	2.00e-58
CAA24998.1	insulin-like growth factor 1A precursor	223	2.00e-58
AAA52538.1	insulin-like growth factor precursor IA	223	2.00e-58
AAA52787.1	insulin-like growth factor precursor	223	2.00e-58

AAA52543.1	insulin-like growth factor I precursor	1.00e-220	57
1203258A	insulin-like growth factor I cytochrome P450, family 2, subfamily E, polypeptide 1; cytochrome P450, subfamily IIE (ethanol-inducible), polypeptide 1; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; cytochrome P450, subfamily IIE (ethanol-inducible)	1.00e-220	57
NM_021282			
NP_067257.1	Mm.21758 F:2		
NP_000764.1	IIE (ethanol-inducible)	792	0
P05181	CPE1_HUMAN Cytochrome P450 2E1 (CYP1IIE1) (P450-J)	792	0
A31949	cytochrome P450 2E1	792	0
AAA52155.1	cytochrome P450IIE1	792	0
AAA35743.1	cytochrome P450j	792	0
AAF13601.1	AF182276_1 cytochrome P450-2E1	790	0
AAD13753.1	cytochrome P450 2E1	751	0
	cytochrome P450, family 2, subfamily C, polypeptide 19; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase		
NP_000760.1	monooxygenase	557 e-158	
	CPCJ_HUMAN Cytochrome P450 2C19 (CYP1IC19) (P450-11A) (Mephenytoin 4-hydroxylase) (CYP1IC17) (P450-254C)		
P33261	4-hydroxylase	557 e-158	
AAB59426.1	cytochrome	557 e-158	
	cytochrome P450, family 2, subfamily C, polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; microsomal monooxygenase; flavoprotein-linked monooxygenase		
NP_000763.1	flavoprotein-linked monooxygenase	556 e-158	
AAB59356.1	cytochrome	556 e-158	
P33260	CPCI_HUMAN Cytochrome P450 2C18 (CYP1IC18) (P450-6B/29C)	553 e-157	
A61269	cytochrome P450 2C18	553 e-157	

AAA02630.1	cytochrome P-4502C18			553 e-157
BAA00123.1	cytochrome P-450			550 e-156
	cytochrome P450, family 2, subfamily C, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase),			
NP_000762.2	polypeptide 9			550 e-156
	CPC9_HUMAN Cytochrome P450 2C9 (CYP1C9) (P450 PB-1) (P450 MP-4)			
P11712	(S-mephenytoin 4-hydroxylase) (P-450MP)			550 e-156
B38462	S-mephenytoin 4-hydroxylase (EC 1.14.14.-) cytochrome P450 2C9			550 e-156
1313295A	cytochrome P450			550 e-156
F38462	S-mephenytoin 4'-hydroxylase (EC 1.14.14.-) cytochrome P450 2C19			550 e-156
AAB23864.2	cytochrome P-450			545 e-155
NM_009219	Mm.29831			
P49660	3	F:2		670 0.0
	CAB51953.1		dJ753D10.1 (somatostatin receptor 4)	670 0.0
P31391	SSR4_HUMAN Somatostatin receptor type 4 (SS4R)			670 0.0
JN0605	receptor 4			670 0.0
AAA36623.				
1	somatostatin receptor			670 0.0
BAA04106.1	fourth somatostatin receptor subtype			670 0.0
NP_001043.1	somatostatin receptor 4			664 0.0
AAA60565.1	somatostatin receptor			664 0.0
NP_001040.	somatostatin receptor 1; somatostatin receptor isoform 1; G-protein coupled			
1	receptor			432 e-121
P30872	SSR1_HUMAN Somatostatin receptor type 1 (SS1R) (SRIF-2)			432 e-121
A41795	somatostatin receptor 1 - human			432 e-121

AAA58247.			
1	somatostatin receptor isoform 1		432 e-121
AAH35618.			
1	Somatostatin receptor 1		432 e-121
AAP84349.1	somatostatin receptor 1		432 e-121
NP_001044.			
1	somatostatin receptor 5		333 4e-091
P35346	SSR5_HUMAN Somatostatin receptor type 5 (SS5R)		333 4e-091
JN0763	somatostatin receptor 5		333 4e-091
BAA04107.1	fifth somatostatin receptor subtype		333 4e-091
AAB31829.1	somatostatin receptor subtype SS2R5, SRIF receptor subtype SS2R5		333 4e-091
AAL88744.1	somatostatin receptor subtype 5		333 4e-091
CAB56181.1	c349E11.1 (somatostatin receptor 5)		333 4e-091
AAK61266.1	somatostatin receptor type 5		333 4e-091
I57955	somatostatin receptor		333 4e-091
AAA20828.1	somatostatin receptor		333 4e-091
AAH09522.1	Unknown (protein for IMAGE:3354783)		333 4e-091
NP_001041.			326 4e-089
1	somatostatin receptor 2		326 4e-089
P30874	SSR2_HUMAN Somatostatin receptor type 2 (SS2R) (SRIF-1)		326 4e-089
B41795	somatostatin receptor 2		326 4e-089
AAA58248.			
1	somatostatin receptor isoform 2		326 4e-089
AAF42809.1	somatostatin receptor 2A		326 4e-089

AAH19610.				
1		Somatostatin receptor 2		326 4e-089
BAC06126.1 seven transmembrane helix receptor				326 4e-089
AAO92064.				
1		somatostatin receptor 2		326 4e-089
AAF42810.1 somatostatin receptor 2B				326 4e-089
NP_004740.				
2		cell cycle progression 2 protein isoform 1		243 1e-064
AAH14918.				
1		Cell cycle progression 2 protein, isoform 1		243 1e-064
AAH17235.				
1		Cell cycle progression 2 protein, isoform 1		243 1e-064
CAD38700.1 hypothetical protein				243 1e-064
AAH02732.2 CPR2 protein				243 1e-064
AAB69312.1 ell cycle progression 2 protein				230 6e-061

MASTER TABLE 1: Subtable 1B Unfavorable Genes/Proteins

Mouse Gene	Human Protein	Behavior	Unigene	Human Protein Name	Score	E-value
AK015750				Chain A, Crystal Structure Of Human Estrogen Sulfotransferase V269e Mutant In The Presence Of Paps	497	e-140
NP_075624	pdh 1HY3 A	U:-7.39	Mm.89655	Chain B, Crystal Structure Of Human Estrogen Sulfotransferase V269e Mutant In The Presence Of Paps	497	e-140
	pdh 1HY3 B			sulfotransferase, estrogen-preferring; estrogen sulfotransferase; estrone sulfotransferase	494	e-139
	NP_005411.1			Estrogen sulfotransferase (Sulfotransferase, estrogen-preferring) (EST-1)	494	e-139
	P49888			estrogen sulfotransferase (EC 2.8.2.-) - human	494	e-139
	JC2229			Chain A, Crystal Structure Of Human Estrogen Sulfotransferase In Complex With In-Active Cofactor Pap And 3,5,3',5'- Tetrachloro-Biphenyl-4,4'-Diol	494	e-139
	pdh 1G3M A			Chain B, Crystal Structure Of Human Estrogen Sulfotransferase In Complex With In-Active Cofactor Pap And 3,5,3',5'- Tetrachloro-Biphenyl-4,4'-Diol	494	e-139
	pdh 1G3M B			estrogen sulfotransferase	494	e-139
	AAA82125.1			estrogen sulfotransferase; hEST-1	494	e-139
	AAB34601.1			estrogen sulfotransferase	494	e-139
	AAC50286.1			estrogen sulfotransferase	494	e-139
	CAA72079.1			estrogen sulfotransferase	494	e-139
	AAQ97179.1			sulfotransferase, estrogen-preferring	494	e-139
	AAH27956.1			Sulfotransferase, estrogen-preferring	492	e-139
				sulfotransferase family, cytosolic, 1B, member 1; thyroid hormone sulfotransferase;		
	NP_055280.2			sulfotransferase 1B1; sulfotransferase 1B2	323	5e-088
	AAB65154.1			thyroid hormone sulfotransferase	323	5e-088
	JC5885			thyroid hormone sulfotransferase (EC 2.8.2.-) B2 - human	323	5e-088
	BAA24547.1			ST1B2	323	5e-088
	AAH10895.1			Sulfotransferase family, cytosolic, 1B, member 1	322	1e-087
	JC2523			aryl sulfotransferase (EC 2.8.2.1) brain isoform - human	315	1e-085
	AAA67895.1			phenol sulfotransferase	315	1e-085

NP_001046.2	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1 isoform a; phenol-preferring phenol sulfotransferase1; phenol-sulfating phenol sulfotransferase; aryl sulfotransferase; thermostable phenol sulfotransferase1	314 2e-085
NP_803565.1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1 isoform a; phenol-preferring phenol sulfotransferase1; phenol-sulfating phenol sulfotransferase; aryl sulfotransferase; thermostable phenol sulfotransferase1	314 2e-085
NP_803566.1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1 isoform a; phenol-preferring phenol sulfotransferase1; phenol-sulfating phenol sulfotransferase; aryl sulfotransferase; thermostable phenol sulfotransferase1	314 2e-085
NP_803878.1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1 isoform a; phenol-preferring phenol sulfotransferase1; phenol-sulfating phenol sulfotransferase; aryl sulfotransferase; thermostable phenol sulfotransferase1	314 2e-085
P50225	Phenol-sulfating phenol sulfotransferase 1 (P-PST) (Thermostable phenol sulfotransferase)	313 3e-085
S52794	sulfotransferase (Ts-PST) (HAST1/HAST2) (ST1A3)	313 3e-085
CAA55089.1	aryl sulfotransferase (EC 2.8.2.1) - human	313 3e-085
CAA07495.1	aryl sulfotransferase	313 3e-085
2021280C	phenol sulfotransferase	313 3e-085
S52791	aryl sulfotransferase	313 3e-085
AAB31316.1	aryl sulfotransferase (EC 2.8.2.1) - human	313 5e-085
CAA55088.1	aryl sulfotransferase ST1A2 [human, liver, Peptide, 295 aa]	313 5e-085
2021280B	aryl sulfotransferase	313 5e-085
NM_026346		
NP_080622		
.1	Mm.40466 U:+6.12 NP_478136.1 F-box only protein 32 isoform 1; muscle atrophy F-box protein; atrogin-1	710 0
	Q969P5 FX32_HUMAN F-box only protein 32 (Muscle atrophy F-box protein) (MAFbx) (Atrogin-1)	710 0

AK006407	***	Mm.45612	U:+5.25	AAL16407.1	muscle atrophy F-box protein	710	0
				BAB71333.1	unnamed protein product	710	0
				CAD12251.1	F-box only 32	710	0
				BAB85128.1	F-box domain Fbx25-containing protein	446	e-124
				NP_680482.1	F-box only protein 32 isoform 2; muscle atrophy F-box protein; atrogin-1	422	e-117
NM_008860	JC1480	Mm.28561	U:+3.52	AAH24030.1	similar to RIKEN cDNA 4833442G10 gene (H. sapiens)	417	e-116
				AAF04526.1	AF174605_1 F-box protein Fbx25	354	-97
				NP_036305.1	F-box only protein 25; F-box protein Fbx25	353	-97
				AAH29237.1	Unknown (protein for IMAGE:5172399)	279	4e-075
				NP_857594.1	hypothetical protein LOC128344	191	9e-075
				BAB85081.1	unnamed protein product	191	9e-075
				NP_002735.2	protein kinase C, zeta	1171	0
				Q05513	Protein kinase C, zeta type (nPKC-zeta)	1171	0
				JN0877	protein kinase C (EC 2.7.1.-) zeta - human	1170	0
				AAA36488.1	protein kinase C zeta	1170	0
				AAH08058.1	Protein kinase C, zeta	1169	0
				AAH14270.1	Protein kinase C, zeta	1169	0
				AAP35745.1	Protein kinase C, zeta	1169	0
				CAA78813.1	protein kinase C zeta	1154	0
				KPCI_HUMAN	Protein kinase C, iota type (nPKC-iota) (Atypical protein kinase		
				P41743	C-lambda/iota) (aPKC-lambda/iota)	876	0
				A49509	protein kinase C (EC 2.7.1.-) iota - human	876	0
				AAA60171.1	protein kinase C iota	876	0
				AAB17011.1	protein kinase C iota	876	0
				NP_002731.2	protein kinase C, iota	871	0

AAH22016.1	Protein Kinase C, iota	871	0
NP_005391.1	protein kinase C, epsilon	399	e-110
Q02156	Protein kinase C, epsilon type (nPKC-epsilon)	399	e-110
S28942	protein kinase C (EC 2.7.1.-) epsilon - human	399	e-110
CAA46388.1	protein kinase C epsilon	399	e-110
NP_006246.2	protein kinase C, eta	384	e-106
AAH37268.1	Protein kinase C, eta	384	e-106
P24723	Protein kinase C, eta type (nPKC-eta) (PKC-L)	382	e-105
A39666	protein kinase C (EC 2.7.1.-) eta - human	382	e-105
AAA60100.1	protein kinase C-L	382	e-105
P05771	Protein kinase C, beta type (PKC-beta) (PKC-B)	367	e-101
KIHUC1	protein kinase C (EC 2.7.1.-) beta-I - human	367	e-101
CAA29634.1	PKC beta 1 (AA 1-671)	367	e-101
NM_013737			
NP_038765	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma);	588	e-168
.1	Platelet-activating factor acetylhydrolase		
Mm.9277	PAFA_HUMAN Platelet-activating factor acetylhydrolase precursor (PAF		
NP_005075.1	acetylhydrolase) (PAF 2-acylhydrolase) (LDL-associated phospholipase A2)		
U:+3.16	(LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine esterase)		
Q13093	(1-alkyl-2-acetyl-glycerophosphocholine esterase)	588	e-168
S60247	platelet-activating factor acetylhydrolase precursor	588	e-168
AAC50126.1	platelet-activating factor acetylhydrolase	588	e-168
2109384A	platelet-activating factor acetylhydrolase	588	e-168
AAB04170.1	LDL-phospholipase A2	587	e-167
AAH38452.1	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	587	e-167
	platelet-activating factor acetylhydrolase 2; platelet-activating factor acetylhydrolase	3.000e	
NP_000428.2	2 (40kD)	287	-77

NM_011618	Q99487	PAF2_HUMAN Platelet-activating factor acetylhydrolase 2, cytoplasmic (Serine dependent phospholipase A2) (HSD-PLA2)	287	-77	3.000e
	BAA13468.1	platelet-activating factor acetylhydrolase 2	287	-77	3.000e
	AAH01158.1	platelet-activating factor acetylhydrolase 2 (40kD)	287	-77	3.000e
	AAC39707.1	serine dependent phospholipase	285	-77	9.000e
NP_035748					1.000e
	1	U: +3.08 Mm.711	267	-71	
	AAB30272.1	troponin T; TnT	267	-71	1.000e
	CAA09751.1	slow skeletal muscle troponin T	267	-71	1.000e
	AAH10963.1	Similar to troponin T1, skeletal, slow	267	-71	1.000e
	AAH34143.1	troponin T1, skeletal, slow	267	-71	1.000e
	NP_003274.1	troponin T1, skeletal, slow; Troponin-T1, skeletal, slow	267	-71	1.000e
	AAH61205.1	slow skeletal muscle troponin T	267	-71	1.000e
	AAB30273.1	troponin T slow isoform; TnT slow isoform	267	-71	1.000e
	CAA09750.1	slow skeletal muscle troponin T	267	-71	1.000e
	AAH22086.1	troponin T1, skeletal, slow	267	-71	1.000e

NIM_026580	AAAG1204.1	slow skeletal muscle troponin T	257	-68	2.000e
	P13805	TRT1_HUMAN Troponin T, slow skeletal muscle isoforms (Slow skeletal muscle troponin T)	257	-68	2.000e
	TPHUTW	troponin T, slow skeletal muscle	257	-68	2.000e
	CAA09752.1	slow skeletal muscle troponin T	257	-68	2.000e
			257	-68	
NP_080856	NP_075601.1	ubiquitin-specific protease otubain 2	449	e-126	
	BAB15172.1	unnamed protein product	449	e-126	
	AAO27703.1	ubiquitin-specific protease otubain 2	449	e-126	
					3.000e
	AAH07519.1	Unknown (protein for MGC:4584)	221	-57	3.000e
	AAO27702.1	ubiquitin-specific protease otubain 1	221	-57	3.000e
	AAF28941.1	AF161381_1 HSPC263	221	-57	3.000e
	NP_060140.1	ubiquitin-specific protease otubain 1	220	-57	7.000e
	BAA90956.1	unnamed protein product	220	-57	7.000e
	AAH10368.1	Unknown (protein for MGC:13444)	220	-57	1.000e
			219	-56	

B Chain B, Crystal Structure Of Human Estrogen Sulfotransferase V269e Mutant In

1HY3	The Presence Of Paps	497 e-140
NP_005411.1	sulfotransferase, estrogen-preferring; estrogen sulfotransferase	494 e-139
P49888	SUOE_HUMAN Estrogen sulfotransferase (Sulfotransferase, estrogen-preferring)	
JC2229	(EST-1)	494 e-139
AAA82125.1	estrogen sulfotransferase (EC 2.8.2.-)	494 e-139
AAB34601.1	estrogen sulfotransferase	494 e-139
AAC50286.1	estrogen sulfotransferase; hEST-1	494 e-139
CAA72079.1	estrogen sulfotransferase	494 e-139
AAH27956.1	estrogen sulfotransferase	492 e-139
	sulfotransferase, estrogen-preferring	4.000e
AAB65154.1	thyroid hormone sulfotransferase	323 -88
		4.000e
JC5885	thyroid hormone sulfotransferase (EC 2.8.2.-) B2	323 -88
		4.000e
BAA24547.1	ST1B2	323 -88
		9.000e
AAH10895.1	Unknown (protein for MGC:13356)	322 -88
		1.000e
JC2523	aryl sulfotransferase (EC 2.8.2.1) brain isoform	315 -85
		1.000e
AAA67895.1	phenol sulfotransferase	315 -85
	SUP1_HUMAN Phenol-sulfating phenol sulfotransferase 1 (P-PST) (Thermostable	2.000e
P50225	phenol sulfotransferase) (Ts-PST) (HAST1/HAST2) (ST1A3)	313 -85
		2.000e
S52794	aryl sulfotransferase (EC 2.8.2.1)	313 -85

NM_009994	CAA55089.1	aryl sulfotransferase	313	-85	2.000e
	CAA07495.1	phenol sulfotransferase	313	-85	2.000e
	2021280C	aryl sulfotransferase	313	-85	2.000e
	S52791	aryl sulfotransferase (EC 2.8.2.1)	313	-85	4.000e
	AAB31316.1	aryl sulfotransferase ST1A2 [human, liver, Peptide, 295 aa]	313	-85	4.000e
	CAA55088.1	aryl sulfotransferase	313	-85	4.000e
	2021280B	aryl sulfotransferase	313	-85	4.000e
	I57945	phenol-sulfating phenol sulfotransferase	313	-85	4.000e
	AAA99892.1	phenol-sulfating phenol sulfotransferase	313	-85	4.000e
	AAC50480.1	phenol sulfotransferase cytochrome P450, family 1, subfamily B, polypeptide 1; aryl hydrocarbon hydroxylase; cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary Infantile); microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	313	-85	4.000e
NP_034124 Mm.214016 U:-2.73	NP_000095.1	monooxygenase; flavoprotein-linked monooxygenase	785	0	
	Q16678	Cytochrome P450 1B1 (CYP1B1)	785	0	
	A54116	cytochrome P450 1B1 - human	785	0	
	AAA19567.1	cytochrome P450	785	0	
	AAH12049.1	Cytochrome P450, family 1, subfamily B, polypeptide 1	785	0	

AAC50809.1	cytochrome P450 CYP1B1	785	0
AAM50512.1	cytochrome P450 CYP1B1	785	0
AAQ87875.1	cytochrome P450, family 1, subfamily B, polypeptide 1 cytochrome P450, family 1, subfamily A, polypeptide 1; aryl hydrocarbon hydroxylase; cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1; flavoprotein-linked monooxygenase; cytochrome P1-450, dioxin-inducible; P450 form 6; xenobiotic monooxygenase; microsomal monooxygenase	785	0
NP_000490.1	monooxygenase	324	8e-088
P04798	Cytochrome P450 1A1 (CYP1A1) (P450-P1) (P450 form 6) (P450-C) aryl hydrocarbon (benzo[a]pyrene) hydroxylase (EC 1.14.14.-) cytochrome P450	324	8e-088
O4HU6	1A1 - human	324	8e-088
CAA27843.1	P-450 c	324	8e-088
AAK25727.1	cytochrome P450	324	8e-088
AAH23019.1	Cytochrome P450, family 1, subfamily A, polypeptide 1	324	8e-088
AAA52139.1	cytochrome P-450-1	322	3e-087
CAA26458.1	cytochrome P(1)-450 cytochrome P450, family 1, subfamily A, polypeptide 2; cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2; dioxin-inducible P3-450; P450 form 4; xenobiotic monooxygenase; aryl hydrocarbon hydroxylase; microsomal monooxygenase; flavoprotein-linked monooxygenase	322	5e-087
NP_000752.1	monooxygenase; flavoprotein-linked monooxygenase	310	1e-083
P05177	Cytochrome P450 1A2 (CYP1A2) (P450-P3) (P(3)450) (P450 4)	310	1e-083
O4HU4	cytochrome P450 1A2 - human	310	1e-083
CAA77335.1	unnamed protein product	310	1e-083
AAA52146.1	cytochrome P3-450	310	1e-083
AAA52163.1	cytochrome P450	310	1e-083
1918405A	cytochrome P450 1A2	310	1e-083
AAK25728.1	cytochrome P450	310	1e-083
AAF13599.1	cytochrome P450-1A2	309	4e-083
AAA35738.1	cytochrome P450 4	308	6e-083

NM_011579	NP_898898.1			cytochrome P450 P450TEC		231	7e-060
	AAQ21380.1			cytochrome P450		231	7e-060
NP_035709							4.000e
	.1	Mm.15793	U:+2.72	NP_062558.1	hypothetical protein R30953_1	233	-61
NM_013703							4.000e
				AAC34467.1	R30953_1	233	-61
NP_038731							
	.1	Mm.4141	U:+2.61	NP_003374.1	very low density lipoprotein receptor	1670	0
	P98155			LDVR_HUMAN	Very low-density lipoprotein receptor precursor (VLDL receptor)	1670	0
	A49729				VLDL receptor precursor, long splice form	1670	0
	BAA03945.1				very low density lipoprotein receptor	1670	0
	BAA03969.1				very low density lipoprotein receptor	1670	0
	AAB31735.1				very low density lipoprotein receptor; VLDL receptor	1670	0
	AAA61344.1				very low density lipoprotein receptor	1668	0
	AAA53684.1				very low density lipoprotein receptor	1665	0
	BAA03946.1				very low density lipoprotein receptor	1610	0
	BAC03874.1				unnamed protein product	1407	0
	NP_000518.1				low density lipoprotein receptor precursor; LDL receptor; LDLR precursor	830	0
	P01130			LDLR_HUMAN	Low-density lipoprotein receptor precursor (LDL receptor)	830	0
	QRHULD				LDL receptor precursor	830	0
	AAA56833.1				low density lipoprotein receptor	830	0
	AAH14514.1				Similar to low density lipoprotein receptor (familial hypercholesterolemia)	830	0
	AAM56036.1				low density lipoprotein receptor	830	0
	AAF24515.1				low density lipoprotein receptor	827	0
	NP_004622.1				apolipoprotein E receptor 2 isoform 1 precursor; apolipoprotein E receptor 2	784	0

NM_025681	BAA09328.1	apolipoprotein E receptor 2 precursor	784	0
	BAA21824.1	ApoER2	784	0
	1N7D	A Chain A, Extracellular Domain Of The Ldl Receptor	768	0
	NP_059992.2	apolipoprotein E receptor 2 isoform 3 precursor; apolipoprotein E receptor 2	661	0
NP_079957				
.1				
	Mm.13130	U:-2.59		
	NP_694966.1	hypothetical protein FLJ25534	493 e-139	
	BAC05298.1	unnamed protein product	493 e-139	
AAH36467.1		Unknown (protein for MGC:33866)	489 e-138	
			3.000e	
	NP_714924.1	hypothetical protein MGC46719	300	-81
			3.000e	
AAH35727.1		Similar to limb expression 1 homolog (chicken)	300	-81
AK003566				
BAB22862.				
1				
	Mm.27159	U:-2.58		
	NP_057234.2	ankyrin repeat and SOCS box-containing protein 2; ankyrin repeat-containing protein ASB-2; ankyrin repeat and SOCS box-2 containing protein	327	-89
			1.000e	
Q96Q27		ASB2_HUMAN Ankyrin repeat and SOCS box containing protein 2 (ASB-2)	327	-89
			1.000e	
CAC17765.1		hypothetical protein	327	-89
			1.000e	
BAB64532.1		ankyrin repeat-containing protein with a SOCS box-2	327	-89
			1.000e	
AAH32354.1		ankyrin repeat and SOCS box-containing 2	327	-89
			1.000e	
T46507		hypothetical protein DKFZp586M2121.1	327	-89

Accession	Protein Name	Length	Score	E-value
CAB70899.1	hypothetical protein	327	-89	1.000e
AAD45345.1	AF159164_1 ankyrin repeat-containing protein ASB-2	319	-87	4.000e
NM_020033				
NP_064417				
NP_065082.1	ankyrin repeat domain 2 (stretch responsive muscle); ankyrin-repeat protein ANR2_HUMAN Ankyrin repeat domain protein 2 (Skeletal muscle ankyrin repeat protein) (hArpp)	541	e-154	
Q9GZV1	ankyrin-repeat protein, Arpp	541	e-154	
JC7713	skeletal muscle ankyrin repeat	541	e-154	
CAC19411.1	skeletal muscle ankyrin protein 2	541	e-154	
CAC19412.1	ankyrin-repeat protein	541	e-154	
BAB60958.1	Similar to ankyrin repeat domain 2 (stretch responsive muscle)	443	e-124	
AAH20817.1	unnamed protein product	281	-75	1.000e
BAB71334.1	bA320F15.2 (nuclear protein similar to CARP)	250	-66	2.000e
CAC70101.1	Unknown (protein for MGC:27140)	250	-66	2.000e
AAH18667.1	cardiac ankyrin repeat protein; cytokine inducible nuclear protein	249	-66	6.000e
NP_055206.1	cytokine inducible nuclear protein C193	249	-66	6.000e
A57291	nuclear protein	249	-66	6.000e
CAA58676.1		249	-66	6.000e

AK003083	NP_659431.3	diabetes related ankyrin repeat protein; muscle ankyrin repeat protein 3	211	2.000e
	AAO24067.1	AF492401_1 diabetes related ankyrin repeat protein	211	2.000e
	AAO40750.1	muscle ankyrin repeat protein 3	211	2.000e
Q8VCK7	XP_351194	similar to syncollin	191	5.000e
	Mm.25210		191	5.000e
	XP_371167	similar to syncollin	191	5.000e
AK019795	XP_372760.1	similar to Hypothetical protein DJ1198H6.2	444	e-124
	O95522	Hypothetical protein DJ1198H6.2	444	e-124
	XP_372762.1	similar to Hypothetical protein DJ1198H6.2	436	e-122
NP_113554	XP_291625.1	similar to Hypothetical protein DJ845O24.2	427	e-119
	XP_291638.1	similar to Hypothetical protein DJ845O24.2	427	e-119
	XP_291396.2	similar to Hypothetical protein DJ845O24.2	424	e-118
.1	O60810	Hypothetical protein DJ845O24.2	420	e-117
		dJ845O24.2 (Melanoma Preferentially Expressed Antigen PRAME and KIAA0014		
	CAA17877.1	LIKE)	420	e-117
AK019795	CAB41253.1	hypothetical protein	420	e-117
		preferentially expressed antigen in melanoma; melanoma antigen preferentially		
		expressed in tumors; Opa-Interacting protein OIP4; preferentially expressed antigen		
NP_006106.1		of melanoma	404	e-112
		Melanoma antigen preferentially expressed in tumors (Preferentially expressed		
		antigen of melanoma) (OPA-interacting protein 4) (OIP4)	404	e-112
P78395		preferentially expressed antigen of melanoma	404	e-112
AAC51160.1				

NM_021347	AAH14074.1	PRAME protein	404	e-112
	AAH39731.1	PRAME protein	404	e-112
	XP_372764.1	similar to Hypothetical protein DJ845O24.2	399	e-110
	XP_372761.1	similar to Hypothetical protein DJ845O24.2	399	e-110
	O60813	Hypothetical protein DJ845O24.5	372	e-102
NM_067322	CAA17880.1	dJ845O24.5 (Melanoma Preferentially Expressed Antigen PRAME and KIAA0014)	372	e-102
	CAB41252.1	LIKE)	372	e-102
	XP_291394.2	hypothetical protein	372	e-102
	XP_291394.2	similar to Hypothetical protein DJ845O24.5	372	e-102
NM_008161	AAL14426.1	gastric cancer-related protein FKSG9	651	0
	NP_835465.1	gasdermin	651	0
	BAC04790.1	unnamed protein product	651	0
	BAC75636.1	gasdermin	650	0
NM_032187	BAA00525.1	glutathione peroxidase	397	e-110
	CAA41228.1	glutathione peroxidase	397	e-110
	P22352	GSHP_HUMAN Plasma glutathione peroxidase precursor (GSHPx-P) (Extracellular	397	e-110
	JQ0476	glutathione peroxidase) (GPx-P)	397	e-110
	NP_002075.2	glutathione peroxidase (EC 1.11.1.9) 3, precursor	390	e-108
	AAF43005.1	plasma glutathione peroxidase 3 precursor	390	e-108
		extracellular glutathione peroxidase	1.000e	
	NP_001500.1	glutathione peroxidase 5 precursor isoform 1; epididymal androgen-related protein	301	-81

NM_013868	NP_038896	Mm:103612 U:-2.4	O75715	GSHE_HUMAN Epididymal secretory glutathione peroxidase precursor (Epididymis-specific glutathione peroxidase-like protein) (EGLP)	301	-81	1.000e
			CAA06463.1	glutathione peroxidase type 5 (GPX5)	301	-81	1.000e
			CAB71121.1	dJ1186N24.2 (glutathione peroxidase 5 (epididymal androgen-related protein))	301	-81	1.000e
			BAA03864.1	plasma glutathione peroxidase similar to EPIDIDYMAL SECRETORY GLUTATHIONE PEROXIDASE PRECURSOR (EPIDIDYMIS-SPECIFIC GLUTATHIONE PEROXIDASE-LIKE PROTEIN) (EGLP)	281	-75	7.000e
			XP_167146.1		202	-52	6.000e
NP_038896	Mm:103612 U:-2.4	Mm:103612 U:-2.4	NP_055239.1	heat shock 27kDa protein family, member 7 (cardiovascular); cardiovascular heat shock protein; heat shock 27kD protein family, member 7 (cardiovascular)	271	-73	6.000e
			Q9UBY9	HSB7_HUMAN Heat-shock protein, beta-7 (Cardiovascular heat shock protein) (cvHsp)	271	-73	6.000e
			CAB63258.1	heat shock protein	271	-73	6.000e
			AAF20022.1	AF155908_1 cardiovascular heat shock protein	271	-73	6.000e
			AAH06319.1	heat shock 27kD protein family, member 7 (cardiovascular)	271	-73	1.000e
			BAC03846.1	unnamed protein product	260	-69	

NM_024283
NP_077245
Mm.274301 U:+2.4 NP_115787.1 esophageal cancer related gene 4 protein 236 3e-062
AAG42321.1 esophageal cancer related gene 4 protein 236 3e-062
AAH21742.1 ECRG4 protein 236 3e-062
AAQ88964.1 ECRG4 236 3e-062
NM_008706
U:+2.37 NP_000894.1 NAD(P)H menadione oxidoreductase 1, dioxin-inducible; diaphorase-4; diaphorase (NADH/NADPH); NAD(P)H:menadione oxidoreductase 1, dioxin-inducible 1; diaphorase (NADH/NADPH) (cytochrome b-5 reductase) NQO1_HUMAN NAD(P)H dehydrogenase [quinone] 1 (Quinone reductase 1) (QR1) (DT-diaphorase) (DTD) (Azoreductase) (Phylloquinone reductase) (Menadiene reductase) 472 e-133
P15559 NAD(P)H2 dehydrogenase (quinone) (EC 1.6.99.2) 1 472 e-133
A30879 NAD(P)H:menadione oxidoreductase 472 e-133
AAA59940.1 NAD(P)H:quinone oxioreductase 472 e-133
AAB60701.1 diaphorase (NADH/NADPH) (cytochrome b-5 reductase) 472 e-133
AAH07659.1 A Chain A, Crystal Structure Of Human Nad[p]h-Quinone Oxidoreductase Co With 2,5-Diaziridinyl-3-Hydroxyl-6-Methyl-1,4-Benzoquinone 471 e-132
1H66 B Chain B, Crystal Structure Of Human Nad[p]h-Quinone Oxidoreductase Co With 2,5-Diaziridinyl-3-Hydroxyl-6-Methyl-1,4-Benzoquinone 471 e-132
1H66 C Chain C, Crystal Structure Of Human Nad[p]h-Quinone Oxidoreductase Co With 2,5-Diaziridinyl-3-Hydroxyl-6-Methyl-1,4-Benzoquinone 471 e-132
1H66 D Chain D, Crystal Structure Of Human Nad[p]h-Quinone Oxidoreductase Co With 2,5-Diaziridinyl-3-Hydroxyl-6-Methyl-1,4-Benzoquinone 471 e-132
1H69 A Chain A, Crystal Structure Of Human Nad[p]h-Quinone Oxidoreductase Co With 2,3,5,6-Tetramethyl-P-Benzooquinone (Duroquinone) At 2.5 Angstrom Resolution 471 e-132

1H69	B Chain B, Crystal Structure Of Human Nad[p]h-Quinone Oxidoreductase Co With 2,3,5,6-Tetramethyl-P-Benzoquinone (Duroquinone) At 2.5 Angstrom Resolution	471 e-132
1H69	C Chain C, Crystal Structure Of Human Nad[p]h-Quinone Oxidoreductase Co With 2,3,5,6-Tetramethyl-P-Benzoquinone (Duroquinone) At 2.5 Angstrom Resolution	471 e-132
1H69	D Chain D, Crystal Structure Of Human Nad[p]h-Quinone Oxidoreductase Co With 2,3,5,6-Tetramethyl-P-Benzoquinone (Duroquinone) At 2.5 Angstrom Resolution	471 e-132
1QBG	A Chain A, Crystal Structure Of Human Dt-Diaphorase (Nad(P)h Oxidoreductase)	470 e-132
1QBG	B Chain B, Crystal Structure Of Human Dt-Diaphorase (Nad(P)h Oxidoreductase)	470 e-132
1QBG	C Chain C, Crystal Structure Of Human Dt-Diaphorase (Nad(P)h Oxidoreductase)	470 e-132
1QBG	D Chain D, Crystal Structure Of Human Dt-Diaphorase (Nad(P)h Oxidoreductase)	470 e-132
1D4A	A Chain A, Crystal Structure Of Human Nad[p]h-Quinone Oxidoreductase At 1.7 A Resolution	470 e-132
1D4A	B Chain B, Crystal Structure Of Human Nad[p]h-Quinone Oxidoreductase At 1.7 A Resolution	470 e-132
1D4A	C Chain C, Crystal Structure Of Human Nad[p]h-Quinone Oxidoreductase At 1.7 A Resolution	470 e-132
1D4A	D Chain D, Crystal Structure Of Human Nad[p]h-Quinone Oxidoreductase At 1.7 A Resolution	470 e-132
1DXO	A Chain A, Crystal Structure Of Human Nad[p]h-Quinone Oxidoreductase Co With 2,3,5,6-Tetramethyl-P-Benzoquinone (Duroquinone) At 2.5 Angstrom Resolution	470 e-132
1DXO	B Chain B, Crystal Structure Of Human Nad[p]h-Quinone Oxidoreductase Co With 2,3,5,6-Tetramethyl-P-Benzoquinone (Duroquinone) At 2.5 Angstrom Resolution	470 e-132
1DXO	C Chain C, Crystal Structure Of Human Nad[p]h-Quinone Oxidoreductase Co With 2,3,5,6-Tetramethyl-P-Benzoquinone (Duroquinone) At 2.5 Angstrom Resolution	470 e-132
1DXO	D Chain D, Crystal Structure Of Human Nad[p]h-Quinone Oxidoreductase Co With 2,3,5,6-Tetramethyl-P-Benzoquinone (Duroquinone) At 2.5 Angstrom Resolution	470 e-132
1GG5	A Chain A, Crystal Structure Of A Complex Of Human Nad[p]h-Quinone Oxidoreductase And A Chemotherapeutic Drug (E09) At 2.5 A Resolution	470 e-132

1GG5	B Chain B, Crystal Structure Of A Complex Of Human Nad[p]h-Quinone Oxidoreductase And A Chemotherapeutic Drug (E09) At 2.5 A Resolution	470 e-132
1GG5	C Chain C, Crystal Structure Of A Complex Of Human Nad[p]h-Quinone Oxidoreductase And A Chemotherapeutic Drug (E09) At 2.5 A Resolution	470 e-132
1GG5	D Chain D, Crystal Structure Of A Complex Of Human Nad[p]h-Quinone Oxidoreductase And A Chemotherapeutic Drug (E09) At 2.5 A Resolution	470 e-132
1KBO	A Chain A, Complex Of Human Recombinant Nad(P)h:quinone Oxide Reductase Type 1 With 5-Methoxy-1,2-Dimethyl-3-(Phenoxyethyl)indole-4,7-Dione (Es1340)	470 e-132
1KBO	B Chain B, Complex Of Human Recombinant Nad(P)h:quinone Oxide Reductase Type 1 With 5-Methoxy-1,2-Dimethyl-3-(Phenoxyethyl)indole-4,7-Dione (Es1340)	470 e-132
1KBO	C Chain C, Complex Of Human Recombinant Nad(P)h:quinone Oxide Reductase Type 1 With 5-Methoxy-1,2-Dimethyl-3-(Phenoxyethyl)indole-4,7-Dione (Es1340)	470 e-132
1KBO	D Chain D, Complex Of Human Recombinant Nad(P)h:quinone Oxide Reductase Type 1 With 5-Methoxy-1,2-Dimethyl-3-(Phenoxyethyl)indole-4,7-Dione (Es1340)	470 e-132
1KBQ	A Chain A, Complex Of Human Nad(P)h Quinone Oxidoreductase With 5-Methoxy-1,2-Dimethyl-3-(4-Nitrophenoxymethyl)indole-4,7-Dione (Es936)	470 e-132
1KBQ	B Chain B, Complex Of Human Nad(P)h Quinone Oxidoreductase With 5-Methoxy-1,2-Dimethyl-3-(4-Nitrophenoxymethyl)indole-4,7-Dione (Es936)	470 e-132
1KBQ	C Chain C, Complex Of Human Nad(P)h Quinone Oxidoreductase With 5-Methoxy-1,2-Dimethyl-3-(4-Nitrophenoxymethyl)indole-4,7-Dione (Es936)	470 e-132
1KBQ	D Chain D, Complex Of Human Nad(P)h Quinone Oxidoreductase With 5-Methoxy-1,2-Dimethyl-3-(4-Nitrophenoxymethyl)indole-4,7-Dione (Es936)	470 e-132
NP_000895.1	NAD(P)H dehydrogenase, quinone 2; NAD(P)H menadione oxidoreductase-1, dioxin-inducible-2; NAD(P)H menadione oxidoreductase 2, dioxin-inducible	224 -58
P16083	NQO2_HUMAN NRH dehydrogenase [quinone] 2 (Quinone reductase 2) (QR2) (NRH:quinone oxidoreductase 2)	224 -58 3.000e
A32667	NAD(P)H2 dehydrogenase (quinone) (EC 1.6.99.2) 2	224 -58 3.000e

NM_008483	AAA60239.1	quinone oxidoreductase	224	3.000e-58
	BAB16974.1	NRH:quinone oxidoreductase 2	224	3.000e-58
	AAH06096.1	NAD(P)H menadione oxidoreductase 2, dioxin-inducible	224	3.000e-58
	AAB60642.2	quinone oxidoreductase2	223	6.000e-58
	1QR2	A Chain A, Human Quinone Reductase Type 2	222	1.000e-57
	1QR2	B Chain B, Human Quinone Reductase Type 2	222	1.000e-57
	2QR2	A Chain A, Human Quinone Reductase Type 2, Complex With Menadione	222	1.000e-57
	2QR2	B Chain B, Human Quinone Reductase Type 2, Complex With Menadione	222	1.000e-57
	NP_002283.2	laminin, beta 2 precursor; laminin S	3201	0
	S53869	laminin beta-2 chain precursor (version 2) - human	3201	0
Q61292	AAB34682.2	laminin beta 2 chain; S-laminin	3201	0
	P55268	Laminin beta-2 chain precursor (S-laminin) (Laminin B1s chain)	3200	0
	CAA92279.1	laminin beta 2 chain	3200	0
	CAA56130.1	beta2/S laminin chain	3127	0
	A55677	laminin beta-2 chain precursor (version 1) - human	3112	0
	NP_002282.1	laminin, beta 1 precursor	1896	0
	P07942	Laminin beta-1 chain precursor (Laminin B1 chain)	1896	0
	MMHUB1	laminin beta-1 chain precursor - human	1896	0
	AAA59482.1	laminin B1	1896	0
	AAA59485.1	laminin B1	1896	0

AAA59486.1	laminin B1	1896	0
XP_209857.3	laminin, beta 4	1352	0
XP_353667.1	similar to laminin beta-4 chain precursor	1352	0
XP_374514.1	similar to laminin beta-4 chain precursor	1352	0
AAC95123.1	laminin beta-4 chain precursor	1349	0
AAH26018.2	LAMB1 protein	959	0
I38231	S-laminin - human (fragment)	914	0
CAA51288.1	S-laminin	914	0
AAF22284.1	laminin beta 1 related protein	731	0
AK007378			
BAB24997.			
1			
Mm.35083	U:+2.36		
NP_077016.1	hypothetical protein MGC4504	379 e-105	
AAH01847.1	Unknown (protein for MGC:4504)	379 e-105	
AAH19625.1	hypothetical protein MGC4504	379 e-105	
NM_008760			
JC4130	Mm.4258		
U:+2.36			
NP_054776.1	osteoglycin preproprotein; osteoinductive factor; mimecan	495 e-139	
NP_077727.1	osteoglycin preproprotein; osteoinductive factor; mimecan	495 e-139	
NP_148935.1	osteoglycin preproprotein; osteoinductive factor; mimecan	495 e-139	
P20774	Mimecan precursor (Osteoglycin) (Osteoinductive factor) (OIF)	495 e-139	
B35272	osteoinductive factor - human	495 e-139	
AAD43022.1	osteoinductive factor OIF	495 e-139	
CAB53706.1	hypothetical protein	495 e-139	
AAF19364.1	mimecan	495 e-139	
AAF69109.1	mimecan	495 e-139	
AAH37273.1	Osteoglycin preproprotein	495 e-139	
AAF97142.1	osteoglycin OG	493 e-193	
CAB61417.1	hypothetical protein	241 6e-063	

				Dermatan sulfate proteoglycan 3 precursor (Epiphycan) (Small		
	Q99645			chondroitin/dermatan sulfate proteoglycan) (Proteoglycan-Lb) (PG-Lb)		215 3e-055
	AAH30958.1			Dermatan sulfate proteoglycan 3		215 3e-055
	NP_004941.1			dermatan sulfate proteoglycan 3; Pg-Lb; dermatan sulphate proteoglycan 3		210 8e-054
	AAC50945.1			dermatan sulfate proteoglycan 3		210 8e-054
	NP_055174.1			opticin; oculoglycan; opticin, oculoglycan		204 8e-052
	Q9UBM4			Opticin precursor (Oculoglycan)		204 8e-052
	AAD45900.1			oculoglycan		204 8e-052
	CAB53459.1			opticin		204 8e-052
	AAL78286.1			opticin		204 8e-052
NM_007570				B-cell translocation gene 2; pheochromocytoma cell-3; NGF-inducible		
Q04211	Mm.239605	U:-2.31		anti-proliferative protein PC3; nerve growth factor-inducible anti-proliferative		304 5e-082
	P78543			BTG2 protein (NGF-inducible anti-proliferative protein PC3)		304 5e-082
	AAB37580.1			BTG2		304 5e-082
	CAA71074.1			NGF-inducible PC3		304 5e-082
	AAL05626.1			BTG2		304 5e-082
	NP_001722.1			B-cell translocation protein 1		211 6e-054
	P31607			BTG1 protein (B-cell translocation gene 1 protein)		211 6e-054
	S20947			BTG1 protein - human		211 6e-054
	CAA43435.1			BTG1		211 6e-054
	AAH16759.1			B-cell translocation protein 1		211 6e-054
	AAH64953.1			B-cell translocation protein 1		211 6e-054
NM_019662						
NP_062636						
.1	Mm.29467	U:-2.3		Ras-related associated with diabetes		486 e-137
	AAA36540.1			Rad		486 e-137
	AAH11645.1			Similar to Ras-related associated with diabetes		486 e-137
	AAB17064.1			Rad GTPase		478 e-135

P55042	RAD_HUMAN GTP-binding protein RAD (RAS associated with diabetes) (RAD1)	454	e-128
A49334	Ras homolog Rad	454	e-128
NP_005252.1	GTP binding protein overexpressed in skeletal muscle; GTP-binding protein expressed in mitogen-stimulated T cells; GTP-binding protein overexpressed in skeletal muscle	298	-81 7.000e
P55040	GEM_HUMAN GTP-binding protein GEM (GTP-binding mitogen-induced T-cell protein) (RAS-like protein KIR)	298	-81 7.000e
A54575	35K GTP-binding protein Gem	298	-81 7.000e
AAA64911.1	Gem	298	-81 7.000e
AAH22010.1	GTP binding protein overexpressed in skeletal muscle	298	-81 8.000e
I38745	kinase-inducible ras-like protein Kir	295	-80 8.000e
AAC50067.1	Ras-like protein; similar to human Gem GTPase, GenBank Accession	295	-80 5.000e
NP_054731.2	RAS (RAD and GEM)-like GTP-binding; GTPase GES; REM protein	249	-66 5.000e
CAB90274.1	dJ1093G12.2 (Ras-like GTP-binding protein REM)	249	-66 5.000e
AAF74212.1	AF152863_1 GTPase GES	249	-66 5.000e
AAH39813.1	RAS (RAD and GEM)-like GTP-binding	249	-66 3.000e
AAC33132.1	Ras-like GTP-binding protein REM	246	-65

similar to GTP-binding protein REM2; Ras-related GTP-binding protein of the Rad/Gem/Kir family [Rattus norvegicus]						2.000e
XP_090793.3					230	-60
unnamed protein product					230	2.000e
BAC04746.1					230	-60
hypothetical protein FLJ38964					230	2.000e
NP_775798.1					230	-60
Similar to Ras-related GTP-binding protein of the Rad/Gem/Kir family, member 2					230	2.000e
AAH35663.1					230	-60
NM_009349						
NP_033375						
.1	Mm.299	U:-2.28	AAD04723.1	thioether S-methyltransferase-like; similar to P40936 (PID:g731019)	271	-73
				INMT_HUMAN indolethylamine N-methyltransferase (Aromatic alkylamine N-methyltransferase) (Indolamine N-methyltransferase) (Arylamine N-methyltransferase) (Amine N-methyltransferase)	267	2.000e
O95050					267	-71
					267	2.000e
AAF18304.1				AF128846_1 indolethylamine N-methyltransferase	267	-71
					267	2.000e
AAF18306.1				AF128848_1 indolethylamine N-methyltransferase	267	-71
					266	4.000e
NP_006765.3				ndolethylamine N-methyltransferase; thioester S-methyltransferase-like	266	-71
					266	4.000e
AAF18305.1				AF128847_1 indolethylamine N-methyltransferase	266	-71
					266	4.000e
AAH33813.1				Unknown (protein for IMAGE:5209218)	266	-71
					239	6.000e
NP_006160.1				nicotinamide N-methyltransferase	239	-63

XP 284174

P15088	CBPC_HUMAN Mast cell carboxypeptidase A precursor (MC-CPA)	3,000e	-76	155
	(Carboxypeptidase A3)	3,000e	-76	
A43929	carboxypeptidase A (EC 3.4.17.1) CPA3 precursor	3,000e	-76	155
AAA35652.1	mast cell carboxypeptidase A precursor	3,000e	-76	155
AAA59568.1	carboxypeptidase A	6,000e	-76	155
AAH12613.1	Similar to carboxypeptidase A3 (mast cell)	7,000e	-75	279
NP_001860.1	carboxypeptidase A2 (pancreatic)	7,000e	-75	279
A56171	carboxypeptidase A2 (EC 3.4.17.15) precursor	7,000e	-75	279
AAA74425.1	preprocarboxypeptidase A2	7,000e	-75	279
P48052	CPB2_HUMAN Carboxypeptidase A2 precursor	7,000e	-75	279
AAH14571.1	Similar to carboxypeptidase A2 (pancreatic)	7,000e	-75	279
AAH15140.1	Unknown (protein for MGC:24316)	7,000e	-75	279
	ras homolog gene family, member B; Aplysia RAS-related homolog 6; oncogene			
NM_007483	RHO H6			
P01121	Transforming protein RhoB (H6)			
TVHURH	GTP-binding protein rhoB - human			
CAA29968.1	rhoB			
AAM21118.1	small GTP binding protein RhoB			

DAA01912.1	TPA: Ras-related small GTPase	402 e-111
DAA01138.1	TPA: Ras-related small GTPase	400 e-111
AAA36565.1	AAA36565.1	347 4e-095
	ras homolog gene family, member A; Aplysia ras-related homolog 12; oncogene	
NP_001655.1	RHO H12	337 4e-092
P06749	Transforming protein RhoA (H12)	337 4e-092
TVHU12	GTP-binding protein rhoA - human	337 4e-092
CAA28690.1	unnamed protein product	337 4e-092
AAC33178.1	GTP-binding protein	337 4e-092
AAH01360.1	ARHA protein	337 4e-092
AAH05976.1	ARHA protein	337 4e-092
AAM21117.1	small GTP binding protein RhoA	337 4e-092
CAE46190.1	CAE46190.1	337 4e-092
	ras homolog gene family, member C; Aplysia RAS-related homolog 9 (oncogene	
	RHO H9); Aplysia ras-related homolog 9; RhoC; RAS homolog gene family,	
NP_786886.1	member C (oncogene RHO H9)	336 1e-091
P08134	Transforming protein RhoC (H9)	336 1e-091
TVHURC	GTP-binding protein rhoC - human	336 1e-091
CAA29969.1	unnamed protein product	336 1e-091
AAC33179.1	GTPase	336 1e-091
AAH07245.1	Ras homolog gene family, member C	336 1e-091
AAH09177.1	Ras homolog gene family, member C	336 1e-091
AAM21119.1	small GTP binding protein RhoC	336 1e-091
AAH52808.1	Ras homolog gene family, member C	336 1e-091
	Chain B, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs In	
pdb 1LB1 B	Complex With Rhoa	335 2e-091
	Chain D, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs In	
pdb 1LB1 D	Complex With Rhoa	335 2e-091

NM_023608	NP_076097	.1	Mm.283495 U:-2.26	Chain F, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs In	335 2e-091
				Complex With Rhoa	335 2e-091
				Chain H, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs In	334 4e-091
				Complex With Rhoa	334 4e-091
				Crystal Structure Of The Human RhoGDP COMPLEX	333 7e-091
				Chain B, Crystal Structure Of Rhoa.Gdp.Mgf3-In Complex With Rhogap	333 7e-091
				Chain A, Crystal Structure Of The Rhoa.Gdp-Rhogdi Complex	331 4e-090
				Chain C, Crystal Structure Of The Rhoa.Gdp-Rhogdi Complex	328 2e-089
				multidrug resistance protein	
				Human Rhoa Complexed With Gtp Analogue	
NP_076097	.1	Mm.283495 U:-2.26	osteoblast differentiation promoting factor protein; lycerophosphodiesterase 3	Chain A, Crystal Structure Of Human Rhoa Complexed With The Effector Domain	328 2e-089
				Of The Protein Kinase PknPRK1	
				osteoblast differentiation promoting factor protein; lycerophosphodiesterase 3	755 0
				phosphodiesterase 3	755 0
				osteoblast differentiation promoting factor	755 0
				Osteoblast differentiation promoting factor protein	755 0
				AESP1935	545 e-166
				unnamed protein product	348 2e-095
				hypothetical protein PP1665	348 2e-095
				unknown	348 2e-095
NP_076097	.1	Mm.283495 U:-2.26	osteoblast differentiation promoting factor protein; lycerophosphodiesterase 3	unknown	348 2e-095
				unknown	348 2e-095
				PP1665 protein	331 4e-090
				hypothetical protein	317 8e-086
				PP1665	290 6e-078
				BAC11242.1	284 4e-076
				unknown	264 5e-070
				PP1665 protein	

AK010249				AAQ72549.1	glycerophosphoryldiester phosphodiesterase UgpQ	252 2e-066
Q61398	Mm.46016	U:-+2.26		NP_037495.1	procollagen C-endopeptidase enhancer 2	709 0
				AAF04621.1	procollagen C-terminal proteinase enhancer protein 2	709 0
				AAK63128.1	procollagen C-proteinase enhancer protein 2	709 0
				AAQ88921.1	PCOLCE2	709 0
				AAH06265.1	PCOLCE2 protein	503 e-142
					Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I procollagen	
					COOH-terminal proteinase enhancer) (Type 1 procollagen C-proteinase enhancer	
				Q15113	protein)	383 e-106
				BAA23281.1	type 1 procollagen C-proteinase enhancer protein	383 e-106
				AAC78800.1	PCOLCE	383 e-106
				AAD16041.1	procollagen C-proteinase enhancer protein	383 e-106
				AAH00574.1	Procollagen C-endopeptidase enhancer	383 e-106
				AAH33205.1	Procollagen C-endopeptidase enhancer	383 e-106
					procollagen C-endopeptidase enhancer; procollagen, type 1, COOH-terminal	
				NP_002584.1	proteinase enhancer	382 e-105
				A55362	procollagen I C-proteinase enhancer protein precursor - human	382 e-105
				AAA61949.1	procollagen C-proteinase enhancer protein	382 e-105
NM_013556						
NP_038584						
.1	Mm.18675	U:-+2.22		NP_000185.1	hypoxanthine phosphoribosyltransferase 1	428 e-120
					HPRT_HUMAN Hypoxanthine-guanine phosphoribosyltransferase (HGPRT)	
				P00492	(HGPRTase)	428 e-120
				RTHUG	hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)	428 e-120
				CAA23789.1	coding sequence	428 e-120
				AAA36012.1	hypoxanthine phosphoribosyltransferase	428 e-120
				AAA52690.1	hypoxanthine phosphoribosyltransferase	428 e-120

AAH00578.1	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	428 e-120
AAB59392.1	hypoxanthine phosphoribosyltransferase	426 e-119
1HMP	A Chain A, Hypoxanthine Guanine Phosphoribosyltransferase (Hgpptase) (E.C.2.4.2.8)	426 e-119
1HMP	B Chain B, Hypoxanthine Guanine Phosphoribosyltransferase (Hgpptase) (E.C.2.4.2.8)	426 e-119
1BZY	A Chain A, Human Hgpptase With Transition State Inhibitor	426 e-119
1BZY	B Chain B, Human Hgpptase With Transition State Inhibitor	426 e-119
1BZY	C Chain C, Human Hgpptase With Transition State Inhibitor	426 e-119
1BZY	D Chain D, Human Hgpptase With Transition State Inhibitor	426 e-119
AAB59391.1	hypoxanthine phosphoribosyltransferase	425 e-119
1009173A	transferase,HG phosphoribosyl	424 e-118
1D6N	A Chain A, Ternary Complex Structure Of Human Hgpptase, Prpp, Mg2+, And The Inhibitor Hpp Reveals The Involvement Of The Flexible Loop In Substrate Binding	417 e-116
1D6N	B Chain B, Ternary Complex Structure Of Human Hgpptase, Prpp, Mg2+, And The Inhibitor Hpp Reveals The Involvement Of The Flexible Loop In Substrate Binding	417 e-116
NP_064585.1	HHGP protein	305 -83
AAF86956.1	HHGP	9,000e
BAB13944.1	unnamed protein product	305 -83
AAH08662.1	HHGP protein	9,000e
BAA12120.1	ficolin	305 -83
NP_001994.2	ficolin 1 precursor; ficolin (collagen/fibrinogen domain-containing) 1	386 e-107
O00602	Ficolin 1 precursor (Collagen/fibrinogen domain-containing protein 1) (Ficollin-A) (Ficollin A) (M-Ficollin)	386 e-107

NM_007995

O70165 Mm.10510 U:-2.2

AAH20635.1	Ficolin 1 precursor	386	e-107
S61517	ficolin-1 precursor - human	382	e-106
AAB50706.1	ficolin	382	e-106
NP_004099.1	ficolin 2 isoform a precursor; ficolin (collagen/fibrinogen domain-containing lectin) 2;	379	e-105
Q15485	ficolin (collagen/fibrinogen domain-containing lectin) 2 (huicolin); huicolin		
BAA08352.1	FCN2_HUMAN Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein	379	e-105
BAA09636.1	2) (Ficolin-B) (Ficolin B) (Serum lectin p35) (EBP-37) (Huicolin) (L-Ficolin)	379	e-105
	serum lectin P35		
	lectin P35		
NP_056652.1	ficolin 2 isoform b precursor; ficolin (collagen/fibrinogen domain-containing lectin) 2;	352	8e-097
	ficolin (collagen/fibrinogen domain-containing lectin) 2 (huicolin); huicolin		
NP_003656.2	ficolin 3 isoform 1 precursor; ficolin-3; collagen/fibrinogen domain-containing lectin 3	289	6e-078
	p35; collagen/fibrinogen domain-containing protein 3; Hakata antigen; H-ficolin		
O75636	Ficolin 3 precursor (Collagen/fibrinogen domain-containing protein 3)	289	6e-078
	(Collagen/fibrinogen domain-containing lectin 3 p35) (Hakata antigen)		
NP_775628.1	ficolin 3 isoform 2 precursor; ficolin-3; collagen/fibrinogen domain-containing lectin 3	281	2e-075
AAQ88448.1	p35; collagen/fibrinogen domain-containing protein 3; Hakata antigen; H-ficolin	258	2e-068
AAQ88678.1	NL3	236	8e-062
	NL7		
NM_008302			
NP_032328	heat shock 90kDa protein 1, beta; heat shock 90kD protein 1, beta; Heat-shock		
.1	90kD protein-1, beta	1202	0
NP_031381.2	HS9B_HUMAN Heat shock protein HSP 90-beta (HSP 84) (HSP 90)	1202	0
P08238	90 kD heat shock protein	1202	0
AAA36026.1	Unknown (protein for MGC:10493)	1202	0
AAH04928.1	Unknown (protein for MGC:3483)	1202	0
AAH12807.1	Unknown (protein for MGC:23206)	1202	0
AAH14485.1	Unknown (protein for MGC:1138)	1202	0
AAH16753.1		1202	0

	HHHU84	heat shock protein 90-beta	1197	0
	AAA36025.1	90kDa heat shock protein	1197	0
	1307197A	heat shock protein 90kD	1197	0
	T46243	hypothetical protein DKFZp761K0511.1	1170	0
	CAB66478.1	hypothetical protein	1170	0
	NP_005339.1	heat shock 90kDa protein 1, alpha; heat shock 90kD protein 1, alpha	1099	0
	HHHU86	heat shock protein 90-alpha	1099	0
	AAA63194.1	heat shock protein	1099	0
	P07900	HS9A_HUMAN Heat shock protein HSP 90-alpha (HSP 86)	1098	0
	CAA33259.1	90 kDa heat-shock protein (AA 1-732)	1098	0
	AAF82792.1	AF275719_1 chaperone protein HSP90 beta	1052	0
	AAH09206.1	heat shock 90kD protein 1, beta	1052	0
	AAH23006.1	Unknown (protein for MGC:30059)	961	0
	AAH00987.1	Unknown (protein for IMAGE:3446372)	800	0
	AAC25497.1	Hsp89-alpha-delta-N	750	0
	AAH07989.1	Similar to heat shock 90kD protein 1, alpha	696	0
K02782				
P01027	AAR89906.1	complement component 3	2550	0
	NP_000055.1	complement component 3 precursor; acylation-stimulating protein cleavage product	2550	0
	P01024	Complement C3 precursor [Contains: C3a anaphylatoxin]	2550	0
	C3HU	complement C3 precursor [validated] - human	2550	0
	AAA85332.1	complement component C3	2550	0
	XP_351177.1	similar to Complement C3 precursor	709	0
	NP_001726.2	complement component 5	658	0
	P01031	Complement C5 precursor [Contains: C5a anaphylatoxin]	658	0
	C5HU	complement C5 precursor [validated] - human	658	0
	AAA51925.1	complement component C5	658	0
	NP_000583.1	complement component 4B proprotein	618	e-176
	AAB67980.1	complement component C4	618	e-176
	CAB89302.1	dJ34F7.4 (complement component 4A)	616	e-175

AA510875	NP_009224.1	complement component 4A preproprotein; acidic C4; Rodgers form of C4; C4A anaphylatoxin	615	e-175
	AAB59537.1	complement component C4A	615	e-175
	C4HU	complement C4A precursor [validated] - human	613	e-175
	AAA51855.1	complement component C4A	613	e-175
NP_613067		chromosome 21 open reading frame 33; human HES1 protein, homolog to E.coli and zebrafish ES1 protein	8.000e	
	NP_004640.1	ES1_HUMAN ES1 protein homolog, mitochondrial precursor (Protein KNP-I)	243	-65
	P30042	(GT335 protein)	8.000e	
	JC4913	anti-sigma cross-reacting protein homolog I alpha precursor	243	-65
	BAA12984.1	KNP-Ia	8.000e	
	AAC50938.1	GT335	243	-65
	AAC50937.1	similar to E. coli SCRP27A and to zebrafish ES1	8.000e	
	AAH02370.1	ES1 (zebrafish) protein, human homolog of	243	-65
	AAH03587.1	ES1 (zebrafish) protein, human homolog of	8.000e	
	CAA68857.1	HES1	243	-65
	BAA95554.1	HES1 protein	8.000e	
			243	-65
			8.000e	

Accession	Gene	Protein	Length	Weight
AK003094	BAA21138.1	KNP-l alpha protein	243	8.000e-65
NP_080390	NP_004085.1	eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kDa); eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD); eukaryotic translation initiation factor 2A; eIF-2-alpha	256	e-113
	P05198	IF2A_HUMAN Eukaryotic translation initiation factor 2 subunit 1 (Eukaryotic translation initiation factor 2 alpha subunit) (eIF-2-alpha) (EIF-2A)	256	e-113
	AAA52373.1	translational initiation factor eIF-2, alpha subunit	256	e-113
	AAH02513.1	eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD)	256	e-113
	CAD61953.1	unnamed protein product	256	e-113
	1KL9	A Chain A, Crystal Structure Of The N-Terminal Segment Of Human Eukaryotic Initiation Factor 2alpha	245	2.000e-64
AK015797				
BAB29981.2	U:+2.18	Similar to RIKEN cDNA 4930515K21 gene	815	0
NM_031396	BAB21793.1	KIAA1702 protein	764	0
NP_113573.1	NP_065081.1	cyclin M1; ancient conserved domain protein 1	1072	0
	AAF86357.1	AF169226_1 ancient conserved domain protein 1	1072	0
	NP_060119.2	cyclin M2; ancient conserved domain protein	597	e-170
	AAF86374.1	ancient conserved domain protein 2	597	e-170
	BAB14386.1	unnamed protein product	596	e-170
	BAB14585.1	unnamed protein product	593	e-169

NM_019824	BAB13418.1	KIAA1592 protein	540	e-153
	NP_064569.1	cyclin M4; ancient conserved domain protein 4	539	e-153
	AAF86370.1	ancient conserved domain protein 4	539	e-153
	BAA90926.1	unnamed protein product	457	e-128
	AAH37272.1	cyclin M3	429	e-119
	NP_060093.2	cyclin M3; ancient conserved domain protein 3	363	e-100
	AAF86377.1	ancient conserved domain protein 3	363	e-100
			6.000e	
	AAH07199.1	Unknown (protein for MGC:12617)	297	-80
NP_062798			365	e-101
	.1	Mm.24498 U:+2.14 NP_005710.1		
		actin related protein 2/3 complex subunit 3; ARP2/3 protein complex subunit p21		
		AR21_HUMAN ARP2/3 complex 21 kDa subunit (P21-ARC) (Actin-related protein		
		2/3 complex subunit 3)	365	e-101
	O15145		365	e-101
	AAB64191.1	p21-Arc	363	e-100
	AAB61466.1	p21-Arc		
		dJ470L14.3 (novel protein similar to the Arp2/3 protein complex subunit p21-Arc	8.000e	
	CAC14083.1	(ARC21))	350	-97
NM_026189		similar to ARP2/3 complex 21 kDa subunit (P21-ARC) (Actin-related protein 2/3	6.000e	
	XP_208062.1	complex subunit 3)	224	-59
NP_080465			1030	0
	.2	Mm.6825 U:+2.14 BAB21797.1		
		KIAA1706 protein		
		NP_085139.1	1030	0
		BAB55076.1	1030	0
		unnamed protein product		

NM_011569

NP_035699	Mm.42257	U: +2.14	NP_444515.1	tektin 1	683	0
			Q969V4	Tektin 1	683	0
			AAH14599.1	Tektin 1	683	0
			AAL27695.1	tektin protein	683	0
			NP_114104.1	tektin 3; testicular microtubules-related protein	291	2e-078
			Q9BXF9	Tektin 3	291	2e-078
			AAK15340.1	testicular microtubules-related protein TEKTN3	291	2e-078
			BAB71464.1	unnamed protein product	290	3e-078
			AAH31688.1	TEKT3 protein	289	7e-078
			NP_653306.1	hypothetical protein MGC27019	273	4e-073
			AAH21716.1	Hypothetical protein MGC27019	273	4e-073
			NP_653275.1	hypothetical protein FLJ32871	267	4e-071
			BAB71484.1	unnamed protein product	267	4e-071
			NP_055281.2	tektin 2; testicular tektin B1-like protein	219	7e-057
			Q9UIF3	Tektin 2 (Tektin-t) (Testicular tektin B1-like protein)	219	7e-057
			BAA89350.1	h-TEKTIN-t	219	7e-057
			CAC21454.1	dJ665N4.3 (novel tektin)	219	7e-057
			AAH35620.1	Tektin 2	219	7e-057
			AAC09343.1	testicular tektin B1-like protein	218	2e-056
D82866					1,000e	
BAA11614.					248	-65
1	Mm.16347	U: +2.13	NP_006219.1	prepronociceptin	1,000e	
			Q13519	PNOC_HUMAN Nociceptin precursor (Orphanin FQ) (PPNOC)	248	-65
			JC6152	orphanin FQ precursor	1,000e	
					248	-65

NM_031388	AAC50651.1	pre-pro-orphanin FQ	248	-65	1.000e
	CAA66039.1	prepronociceptin	248	-65	1.000e
	CAA66040.1	prepronociceptin	248	-65	1.000e
	AAH34758.1	prepronociceptin	248	-65	1.000e
NP_113565	NP_114113.1	ubiquitin-specific protease 26	420	e-117	
	Q9BXU7	UBPQ_HUMAN Ubiquitin carboxyl-terminal hydrolase 26 (Ubiquitin thiolesterase 26) (Ubiquitin-specific processing protease 26) (Deubiquitinating enzyme 26)	420	e-117	
	AAK31972.1	AF285593_1 ubiquitin specific protease 26	420	e-117	
	NP_065954.1	ubiquitin-specific processing protease; likely ortholog of mouse ubiquitin-specific processing protease 29	327	-89	6.000e
	Q9HBJ7	UBPT_HUMAN Ubiquitin carboxyl-terminal hydrolase 29 (Ubiquitin thiolesterase 29) (Ubiquitin-specific processing protease 29) (Deubiquitinating enzyme 29)	327	-89	6.000e
	AAG10401.1	AF229438_1 ubiquitin-specific processing protease	327	-89	6.000e
	XP_050754.5	similar to KIAA1594 protein	280	-74	1.000e
NM_010865	BAB13420.1	KIAA1594 protein	259	-68	
	NP_000252.1	myocilin; trabecular meshwork-induced glucocorticoid response protein	782	0	
	Q99972	Myocilin precursor (Trabecular meshwork-induced glucocorticoid response protein)	782	0	

JC5830	myocilin - human	782	0
AAC52051.1	trabecular meshwork inducible glucocorticoid response protein	782	0
AAC51725.1	trabecular meshwork-induced glucocorticoid response protein	782	0
CAB09899.1	GLC1A	782	0
BAA23531.1	myocilin	782	0
AAC14264.1	myocilin	782	0
AAH29261.1	Myocilin	782	0
BAA24532.1	myocilin	763	0
CAD92590.1	dJ454G6.1 (myocilin, trabecular meshwork inducible glucocorticoid response (TIGR))	763	0
BAC04997.1	unnamed protein product	706	0
NP_477512.1	olfactomedin 2; neuronal olfactomedin related ER localized protein 2; noelin 2	215	2e-055
AAH11361.1	Olfactomedin 2	215	2e-055
O95897	Noelin 2 precursor (Olfactomedin 2)	215	2e-055
AAD20056.1	Human neuronal olfactomedin related ER localized protein	215	2e-055
BAC04756.1	unnamed protein product	213	7e-055
	olfactomedin related ER localized protein isoform 1; neuroblastoma protein;		
NP_055094.1	olfactomedin related ER localized protein; pancortin 1	213	7e-055
AAH08763.2	Olfactomedin related ER localized protein, isoform 1	213	7e-055
AAH11741.2	Olfactomedin related ER localized protein, isoform 1	213	7e-055
	Noelin precursor (Neuronal olfactomedin-related ER localized protein)		
Q99784	(Olfactomedin 1)	211	3e-054
AAP35810.1	olfactomedin 1	211	3e-054
AAH15437.2	AAH15437.2	209	1e-053
	chymase 1, mast cell preproprotein; chymase, mast cell; chymase, heart; mast cell		
NP_001827.1	protease I	345	1e-094
P23946	Chymase precursor (Mast cell protease I)	345	1e-094
KYHUCM	chymase (EC 3.4.21.39) precursor [validated] - human	345	1e-094
AAA52019.1	chymase	345	1e-094
NIM_010780			
S26043	Mm.1252		
	U:-2.13		

AAA52020.1	mast cell chymase	345	1e-094
AAA52021.1	chymase	345	1e-094
1NN6	Chain A, Human Pro-Chymase	342	8e-094
1KLT	Crystal Structure Of Pmsf-Treated Human Chymase At 1.9 Angstroms Resolution	333	2e-091
AAB26828.1	chymase	333	2e-091
1914144A	chymase	333	2e-091
1PJP	A Chain A, The 2.2 A Crystal Structure Of Human Chymase In Complex With Succinyl-Ala-Ala-Pro-Phe-Chloromethylketone	331	1e-090
AF281045			
AAG33708.			
1			
Mm.87471	NP_066956.1	904	0
U:+2.12	ribonuclease L (2',5'-oligoadenylate synthetase-dependent); ribonuclease 4 RN5A_HUMAN 2-5A-dependent ribonuclease (2-5A-dependent RNase)		
Q05823	(Ribonuclease L) (RNase L) (Ribonuclease 4)	904	0
AAA18032.1	2-5A-dependent RNase	904	0
A45771	2-5A-dependent RNAase	900	0
AK016927			
BAB30501.			
1			
Mm.73186	NP_061840.1	403	e-112
U:+2.12	syntrophin, gamma 1; gamma1-syntrophin; syntrophin 4; gamma1-syntrophin		
Q9NSN8	STG1_HUMAN Gamma-1-syntrophin (G1SYN) (Syntrophin 4) (SYN4)	403	e-112
T47134	hypothetical protein DKFZp761I2312.1	403	e-112
CAB82311.1	hypothetical protein	403	e-112
		3.000e	
CAB92968.1	syntrophin 4	333	-91
		5.000e	
NP_061841.1	syntrophin, gamma 2; syntrophin 5; gamma2-syntrophin	219	-57
		5.000e	
Q9NY99	STG2_HUMAN Gamma-2-syntrophin (G2SYN) (Syntrophin 5) (SYN5)	219	-57

NM_013467	CAB92969.1	syntrophin 5	219	5.000e-57
NP_038495				
.1	Mm.4514	U: +2.12	870	0
NP_000680.2		aldehyde dehydrogenase 1		
		aldehyde dehydrogenase 1A1; aldehyde dehydrogenase 1, soluble; aldehyde dehydrogenase, liver cytosolic; ALDH class 1; acetaldehyde dehydrogenase 1; retinal dehydrogenase 1	869	0
P00352		DHA1_HUMAN Aldehyde dehydrogenase 1A1 (Aldehyde dehydrogenase, cytosolic) (ALDH class 1) (ALDHII) (ALDH-E1)	869	0
	DEHUE1	aldehyde dehydrogenase (NAD) (EC 1.2.1.3) 1, cytosolic	869	0
AAA51692.1		aldehyde dehydrogenase	869	0
AAH01505.1		Unknown (protein for MGC:2318)	869	0
NP_003879.2		aldehyde dehydrogenase 1A2 isoform 1; retinaldehyde dehydrogenase 2; retinaldehyde-specific dehydrogenase type 2	719	0
	BAA34785.1	RALDH2	719	0
O94788		DHA2_HUMAN Aldehyde dehydrogenase 1A2 (Retinaldehyde-specific dehydrogenase type 2) (RALDH(II)) (RALDH-2)	717	0
	NP_000684.1	aldehyde dehydrogenase 1A3; aldehyde dehydrogenase 6	686	0
P47895		DHA6_HUMAN Aldehyde dehydrogenase 6	686	0
A55684		aldehyde dehydrogenase (NAD) (EC 1.2.1.3) 6 precursor, salivary	686	0
AAA79036.1		aldehyde dehydrogenase 6	686	0
NP_000681.2		mitochondrial aldehyde dehydrogenase 2 precursor; acetaldehyde dehydrogenase 2; nucleus-encoded mitochondrial aldehyde dehydrogenase 2; liver mitochondrial		
		ALDH; ALDH class 2	657	0
P05091		DHAM_HUMAN Aldehyde dehydrogenase, mitochondrial precursor (ALDH class 2) (ALDH1) (ALDH-E2)	657	0

DEHUE2	aldehyde dehydrogenase (NAD) (EC 1.2.1.3) 2 precursor, mitochondrial	657	0
AAH02967.1	aldehyde dehydrogenase 2, mitochondrial	657	0
1O05	A Chain A, Apo Form Of Human Mitochondrial Aldehyde Dehydrogenase	656	0
1O05	B Chain B, Apo Form Of Human Mitochondrial Aldehyde Dehydrogenase	656	0
1O05	C Chain C, Apo Form Of Human Mitochondrial Aldehyde Dehydrogenase	656	0
1O05	D Chain D, Apo Form Of Human Mitochondrial Aldehyde Dehydrogenase	656	0
1O05	E Chain E, Apo Form Of Human Mitochondrial Aldehyde Dehydrogenase	656	0
1O05	F Chain F, Apo Form Of Human Mitochondrial Aldehyde Dehydrogenase	656	0
1O05	G Chain G, Apo Form Of Human Mitochondrial Aldehyde Dehydrogenase	656	0
1O05	H Chain H, Apo Form Of Human Mitochondrial Aldehyde Dehydrogenase	656	0
AAA51693.1	aldehyde dehydrogenase	655	0
1CW3	A Chain A, Human Mitochondrial Aldehyde Dehydrogenase Complexed With Nad+ And Mn2+	654	0
1CW3	B Chain B, Human Mitochondrial Aldehyde Dehydrogenase Complexed With Nad+ And Mn2+	654	0
1CW3	C Chain C, Human Mitochondrial Aldehyde Dehydrogenase Complexed With Nad+ And Mn2+	654	0
1CW3	D Chain D, Human Mitochondrial Aldehyde Dehydrogenase Complexed With Nad+ And Mn2+	654	0
1CW3	E Chain E, Human Mitochondrial Aldehyde Dehydrogenase Complexed With Nad+ And Mn2+	654	0
1CW3	F Chain F, Human Mitochondrial Aldehyde Dehydrogenase Complexed With Nad+ And Mn2+	654	0
1CW3	G Chain G, Human Mitochondrial Aldehyde Dehydrogenase Complexed With Nad+ And Mn2+	654	0
1CW3	H Chain H, Human Mitochondrial Aldehyde Dehydrogenase Complexed With Nad+ And Mn2+	654	0

NM_022314

NP_071709

.1

Mm.17306	U:-2.12	P06753	TPM3_HUMAN Tropomyosin alpha 3 chain (Tropomyosin 3) (Tropomyosin gamma)	365 e-101
		A24199	tropomyosin NM, skeletal muscle	365 e-101
		CAA27798.1	skeletal muscle tropomyosin (AA 1-285)	365 e-101
		AAH08407.1	Unknown (protein for MGC:14532)	365 e-101
		AAH08425.1	Unknown (protein for MGC:14582)	365 e-101
		1209280A	tropomyosin	8.000e
		P09493	TPM1_HUMAN Tropomyosin 1 alpha chain (Alpha-tropomyosin)	345 -95
		A25825	tropomyosin alpha chain, cardiac and skeletal muscle	8.000e
		AAA61225.1	skeletal muscle tropomyosin	345 -95
		P07951	TPM2_HUMAN Tropomyosin beta chain (Tropomyosin 2) (Beta-tropomyosin)	326 -89
		S00922	tropomyosin beta, skeletal muscle	3.000e
		CAA29971.1	beta-tropomyosin (AA 1-284)	326 -89
		NP_000357.3	tropomyosin 1 (alpha)	6.000e
		AAH07433.1	Similar to tropomyosin 1 (alpha)	325 -89
		NP_689476.1	tropomyosin 3	9.000e
				315 -86

						9.000e
					315	-86
						2.000e
					310	-84
						2.000e
					300	-81
						1.000e
					281	-75
						1.000e
					281	-75
						1.000e
					278	-74
						1.000e
					278	-74
NM_022434						
NP_071879						
.1	Mm.10976	U:+2.12	AAC08589.1	cytochrome P-450	855	0
			BAA75823.1	Leukotriene B4 omega-hydroxylase	855	0
				cytochrome P450, family 4, subfamily F, polypeptide 2; cytochrome P450, subfamily IVF, polypeptide 2; leukotriene B4 omega-hydroxylase; leukotriene-B4		
			NP_001073.3	20-monoxygenase	853	0
				CYP2_HUMAN Cytochrome P450 4F2 (CYP4F2) (Leukotriene-B4		
				omega-hydroxylase) (Leukotriene-B4 20-monoxygenase) (Cytochrome		
			P78329	P450-LTB-omega)	853	0
			S45702	leukotriene-B4 20-monoxygenase (EC 1.14.13.30) cytochrome P450 4F3	853	0
			BAA05490.1	leukotriene B4 omega-hydroxylase	853	0

	CYP4F2; LEUKOTRIENE-B4 20-MONOXYGENASE; YTOCHROME		0
AAC27730.1	P450-LTB-OMEGA; LEUKOTRIENE-B4 OMEGA-HYDROXYLASE	853	0
AAL67578.1	cytochrome P450, subfamily IVF, polypeptide 2	853	0
Q9HBI6	CPFB_HUMAN Cytochrome P450 4F11 (CYP4F11)	848	0
AAH16853.1	cytochrome P450, subfamily IVF, polypeptide 11	848	0
	cytochrome P450, family 4, subfamily F, polypeptide 11; cytochrome P450, subfamily IVF, polypeptide 11		
NP_067010.1	subfamily IVF, polypeptide 11	848	0
AAG15889.1	AF236085_1 CYP4F11	848	0
AAC50052.2	cytochrome P450 4F2	845	0
	cytochrome P450, family 4, subfamily F, polypeptide 3; cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase); leukotriene B4 omega hydroxylase; leukotriene-B4 20-monooxygenase; cytochrome P450-LTB-omega		
NP_000887.1	CPF3_HUMAN Cytochrome P450 4F3 (CYP4F3) (Leukotriene-B4 omega-hydroxylase) (Leukotriene-B4 20-monooxygenase) (Cytochrome P450-LTB-omega)	808	0
	P450-LTB-omega)		
Q08477	leukotriene B4 omega-hydroxylase (EC 1.14.15.-) cytochrome P450	808	0
A46661	cytochrome P-450LTBV	808	0
BAA02144.1	leukotriene B4 omega-hydroxylase	808	0
BAA25990.1	leukotriene B4 omega-hydroxylase	808	0
BAA25991.1	leukotriene B4 omega-hydroxylase	808	0
Q9HCS2	CPFC_HUMAN Cytochrome P450 4F12 (CYP4F12)	807	0
JC7594	cytochrome P450 enzyme, CYP4F12 isoform, liver	807	0
JC7598	cytochrome P450 enzyme, CYP4F12 isoform, small intestine	807	0
BAB18269.1	cytochrome P450	807	0
AAG33247.1	cytochrome P450 isoform 4F12	807	0
	cytochrome P450, family 4, subfamily F, polypeptide 8; cytochrome P450, subfamily IVF, polypeptide 8; microsomal monooxygenase; flavoprotein-linked monooxygenase		
NP_009184.1	monooxygenase	804	0
P98187	CPFB_HUMAN Cytochrome P450 4F8 (CYP4F8)	804	0
AAD49566.1	AF133298_1 cytochrome P450	804	0

NIM_026161	NP_076433.1	4F12; cytochrome P450, subfamily IVF, polypeptide 12	cytochrome P450, family 4, subfamily F, polypeptide 12; cytochrome P450 isoform	803	0
				803	0
NP_080437	BAB18270.1	cytochrome P450		345	e-140
				343	e-139
.1	Mm.258993	U: +2.12	C1q and tumor necrosis factor related protein 4	343	e-139
				343	e-139
AK002873	NP_114115.1	Q9BXJ3	Complement-c1q tumor necrosis factor-related protein 4 precursor	343	e-139
				343	e-139
BAB22421.	NP_115750.1	U: +2.1	hypothetical protein MGC2562	4,000e	
				302	-82
M55181	AAH07412.1	U: +2.1	Similar to RIKEN cDNA 2810002N01 gene	302	-82
				461	e-129
B35678	NP_006202.1	U: +2.1	proenkephalin	461	e-129
				461	e-129
P01210	EQHUA	U: +2.1	Proenkephalin A precursor [Contains: Synenkephalin; Met-enkephalin (Opioid growth factor) (OGF); Met-enkephalin-Arg-Gly-Leu; Leu-enkephalin; Met-enkephalin-Arg-Phe]	461	e-129
				461	e-129
AAB59409.1	AAH32505.1	U: +2.1	preproenkephalin precursor	461	e-129
				461	e-129
0803246A	U: +2.1	U: +2.1	Proenkephalin	461	e-129
				461	e-129

Accession	Gene	Protein	Function	Length	Score
NM_007485					
NP_031511					
1	Mm.27701	U:+2.09	NP_055393.1	ras homolog D; ras homolog gene family, member A; Rho-related protein HP1;	4.000e
				Rho-related GTP-binding protein RhoD	339 -93
				RHOD_HUMAN Rho-related GTP-binding protein RhoD (Rho-related protein HP1)	4.000e
				(RhoHP1)	339 -93
					4.000e
				BAA19652.1	339 -93
				rhoHP1	4.000e
					339 -93
				AAH01338.1	4.000e
				ras homolog gene family, member	339 -93
					4.000e
				AAM21120.1	339 -93
				AF498973_1 small GTP binding protein RhoD	3.000e
				RHOE_HUMAN Rho-related GTP-binding protein RhoF (Rho-family GTPase Rif)	3.000e
				(Rho in filopodia)	210 -54
					3.000e
				AAG24952.1	210 -54
				AF239923_1 Rho family small GTPase	5.000e
					209 -54
				NP_061907.1	5.000e
				ras homolog gene family, member F	209 -54
					5.000e
				BAA91034.1	209 -54
				unnamed protein product	6.000e
				ras homolog gene family, member A; Aplysia ras-related homolog 12; Rho12;	6.000e
				RhoA; Ras homolog gene family, member A (oncogene RHO H12)	196 -50
					6.000e
				P06749	196 -50
				RHOA_HUMAN Transforming protein RhoA (H12)	6.000e
					196 -50
				TVHU12	196 -50
				GTP-binding protein rhoA	6.000e
					196 -50
				CAA28690.1	196 -50
				ORF (AA 1-193)	6.000e

Accession	Protein Name	Length	Score
AAC33178.1	GTP-binding protein	196	6.000e-50
AAH01360.1	ras homolog gene family, member A	196	6.000e-50
AAH05976.1	ras homolog gene family, member A	196	6.000e-50
AAM21117.1	AF498970_1 small GTP binding protein RhoA	196	6.000e-50
1LB1	B Chain B, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs	196	6.000e-50
1LB1	In Complex With Rhoa	196	6.000e-50
1LB1	D Chain D, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs	196	6.000e-50
1LB1	In Complex With Rhoa	196	6.000e-50
1LB1	F Chain F, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs	196	6.000e-50
1LB1	In Complex With Rhoa	196	6.000e-50
1LB1	H Chain H, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs	196	6.000e-50
1LB1	In Complex With Rhoa	196	6.000e-50
AAA50612.1	multidrug resistance protein	196	6.000e-50
BAA84996.1	brain carboxylesterase hBr3	1092	0
BAB85656.1	brain carboxylesterase hBr2	909	0
AAH12418.1	Unknown (protein for MGC:9220)	908	0
NP_001257.3	carboxylesterase 1 (monocyte/macrophage serine esterase 1); carboxylesterase 2 (liver); liver carboxylesterase; cholesterol ester hydrolase	905	0
BAA04650.1	carboxylesterase	904	0
AAA35711.1	carboxylesterase	903	0

AAD53175.1	AF177775_1 egasyn			902	0
	EST1_HUMAN Liver carboxylesterase precursor (Acyl coenzyme A:cholesterol acyltransferase) (ACAT) (Monocyte/macrophage serine esterase) (HMSE) (Serine esterase 1) (Brain carboxylesterase hBr1)				
P23141	carboxylesterase (EC 3.1.1.1) precursor, monocyte/macrophage carboxylesterase			902	0
A41010	acyl coenzyme A:cholesterol acyltransferase			902	0
AAA35649.1	carboxylesterase			902	0
AAC60631.2	acyl coenzyme A:cholesterol acyltransferase			897	0
AAA16036.1	carboxylesterase			894	0
M36654					
AAA37848.					
1					
	Mm.3546	μJ:+2.07			
NP_076920.1	homeo box B4; homeobox protein Hox-B4; homeo box 2F			396 e-110	
P17483	HXB4_HUMAN Homeobox protein Hox-B4 (Hox-2F) (Hox-2.6)			396 e-110	
B60492	homeotic protein Hox B4			396 e-110	
AAG31554.1	AF287967_4 homeobox B4			396 e-110	
AAG45052.1	HOXB4			396 e-110	
T46446	hypothetical protein DKFZp434G0128.1			388 e-107	
CAB70742.1	hypothetical protein			388 e-107	
				7.000e	
NP_055435.2	homeo box C4; homeo box 3E			252	-67
				7.000e	
NP_705897.1	homeo box C4; homeo box 3E			252	-67
				3.000e	
P09017	HXC4_HUMAN Homeobox protein Hox-C4 (Hox-3E) (CP19)			250	-66
				3.000e	
WJHU3E	homeotic protein Hox C4			250	-66
				3.000e	
CAA30376.1	translated/region (AA 1-264)			250	-66
				3.000e	
AAG42145.1	HOXC4			250	-66

	NP_055436.2	X	homeo box D4; homeobox protein Hox-D4; Hox-4.2, mouse, homolog of homeo box	4.000e -60 230
P09016	HXD4_HUMAN	Homeobox protein Hox-D4 (Hox-4B) (Hox-5.1) (HHO.C13)		4.000e -60 230
AAH16763.1	Unknown	(protein for MGC:22628)		4.000e -60 230
WJHU4B	homeotic protein Hox D4			8.000e -60 229
CAA35237.1	hox 5.1 protein			8.000e -60 229
CAA28411.1	put. gene product (AA 1-255)			1.000e -59 228
1301323A	gene homeobox			1.000e -59 228
NP_002132.2	homeobox protein A4; homeobox protein HOX-A4; Hox-1.4-like protein; Dfd-like protein			2.000e -55 214
Q00056	HXA4_HUMAN	Homeobox protein Hox-A4 (Hox-1D) (Hox-1.4)		2.000e -55 214
A39724	homeotic protein Hox A4			4.000e -55 213
AAA58664.1	Hox 1.4			4.000e -55 213
NM_011849				
NP_035979				
.1	Mm.57013	U:+2.04	NIMA (never in mitosis gene a)-related kinase 4; Serine/threonine protein kinase-2; serine/threonine kinase 2	988 0
	P51957		NEK4_HUMAN Serine/threonine-protein kinase NEK4 (NimA-related protein kinase 4) (Serine/threonine protein kinase 2) (Serine/threonine-protein kinase NRK2)	988 0

I78885	serine/threonine-specific protein kinase (EC 2.7.1.-) STK2	988	0
	protein serine/threonine kinase	988	0
AAA36658.1	NEK1_HUMAN Serine/threonine-protein kinase NEK1 (NIMA-related protein kinase 1) (NY-REN-55 antigen)	256	1.000e-67
Q96PY6		256	1.000e-67
BAB67794.1	KIAA1901 protein	224	5.000e-58
NP_002489.1	NIMA-related kinase 3; serine/threonine-protein kinase NEK3; phosphorylase B kinase kinase; glycogen synthase A kinase; hydroxyalkyl-protein kinase	224	5.000e-58
NP_689933.1	NIMA-related kinase 3; serine/threonine-protein kinase NEK3; phosphorylase B kinase kinase; glycogen synthase A kinase; hydroxyalkyl-protein kinase	224	5.000e-58
P51956	NEK3_HUMAN Serine/threonine-protein kinase NEK3 (NIMA-related protein kinase 3) (HSPK 36)	224	3.000e-58
BAC15599.1	NIMA-related protein kinase 3	221	2.000e-53
CAA82310.1	protein kinase	209	3.000e-53
AAH19916.1	Unknown (protein for MGC:29949)	208	-53
NM_021893			
NP_068693		407	e-113
		407	e-113
.1	Mm.168681 U:-2.04	407	e-113
	NP_054862.1 B7-H1 protein	240	-63
	AAF25807.1 AF177937_1 B7-H1		
	AAG18508.1 AF233516_1 PD-1-ligand precursor		
	BAA91966.1 unnamed protein product		

Accession	Gene	Protein	Accession	Gene	Protein	Accession	Gene	Protein	Accession	Gene	Protein
NM_054054											
NP_473395											
NP_001717.1	U: +2.04	Mm.24536	NP_001717.1	testis-specific bromodomain protein	1084	0					
AAB87862.1			BRDT		1084	0					
AAH38844.1			Unknown (protein for IMAGE:5742670)		668	0					
AAH47900.1			Similar to bromodomain, testis-specific		668	0					
CAC69991.1			O14.1.1 (bromodomain-containing protein 2 (RING3, KIAA9001), isoform 1)		545	e-154					
CAC69989.1			O27.1.1 (bromodomain-containing protein 2 (RING3, KIAA9001), isoform 1)		545	e-154					
NP_005095.1			bromodomain containing protein 2; female sterile homeotic-related gene 1		545	e-154					
P25440			BRD2_HUMAN Bromodomain-containing protein 2 (RING3 protein) (O27.1.1)		545	e-154					
BAA07641.1			KIAA9001		545	e-154					
CAA43996.1			FSH		545	e-154					
CAA65450.1			kinase		545	e-154					
A56619			female sterile homeotic (fsh) homolog RING3		545	e-154					
AAA68890.1			putative		545	e-154					
			bromodomain containing protein 3; RING3-like gene; bromodomain-containing 3;								
NP_031397.1			open reading frame X		536	e-152					
Q15059			BRD3_HUMAN Bromodomain-containing protein 3 (RING3-like protein)		536	e-152					
BAA05393.1			KIAA0043		536	e-152					
AAC27978.1			R31546_1		531	e-150					
NP_055114.1			bromodomain-containing protein 4 Isoform short; chromosome-associated protein		531	e-150					
CAA72780.1			strong homology to human RING3 sequence		531	e-150					
AAO22237.1			BRD4-NUT fusion oncoprotein		531	e-150					
AK007200											
None			hypothetical protein LOC375759		208	1e-053					
NM_008393											
P81067			homeodomain protein IRXB1; irx3; irx-1		404	e-112					
			Iroquois-class homeodomain protein IRX-3 (Iroquois homeobox protein 3)		404	e-112					

NM_008687	P97863	Mm.126173 U:-2.04	AAH23667.1	Iroquois homeobox protein 3	404	e-112
			NP_077312.1	iroquois homeobox protein 3	404	e-112
			AAQ16549.1	homeodomain protein IRXB1	404	e-112
NM_008458	S19724	Mm.14191 U:-2.04	AAH01283.1	Nuclear factor I/B	808	0
			AAP35930.1	Nuclear factor I/B	808	0
			NP_005587.1	nuclear factor I/B	806	0
				Nuclear factor 1 B-type (Nuclear factor 1/B) (NF1-B) (NF1-B) (NF-I/B) (CCAAT-box		
			O00712	binding transcription factor) (CTF) (TGGCA-binding protein)	806	0
			AAB41899.1	nuclear factor I-B2	806	0
			AAA93125.1	nuclear factor 1 B-type	506	e-143
			NP_005588.1	nuclear factor I/C (CCAAT-binding transcription factor)	498	e-140
			CAA63440.1	NFI /CAAT-binding transcription factor 5 (CTF5)	498	e-140
			AAH12120.1	Nuclear factor I/C (CCAAT-binding transcription factor)	498	e-140
				Nuclear factor 1 C-type (Nuclear factor 1/C) (NF1-C) (NF1-C) (NF-I/C) (CCAAT-box		
			P08651	binding transcription factor) (CTF) (CCAAT-box binding transcription factor) (CTF)	486	e-137
			B33416	nuclear factor I - human	483	e-136
			BAA92677.1	KIAA1439 protein	483	e-136
				Nuclear factor 1 A-type (Nuclear factor 1/A) (NF1-A) (NF1-A) (NF-I/A) (CCAAT-box		
			Q12857	binding transcription factor) (CTF) (TGGCA-binding protein)	483	e-136
			NP_005586.1	nuclear factor I/A	483	e-136
			AAH22264.1	Nuclear factor I/A	483	e-136
				alpha1-antichymotrypsin	494	e-139
			CAA48671.1	Alpha-1-antichymotrypsin precursor (ACT)	490	e-138
			P01011	SERPINA3 protein	490	e-138
			AAH03559.1	SERPINA3 protein	490	e-138
			AAH10530.1	SERPINA3 protein	490	e-138
			AAH34554.1	SERPINA3 protein	489	e-138
			AAD08810.1	alpha-1-antichymotrypsin precursor	478	e-134

ITHUC	alpha-1-antichymotrypsin precursor - human	476	e-134
AAA51560.1	alpha-1-antichymotrypsin precursor	470	e-132
	Chain A, Alpha1-Antichymotrypsin Serpin In The Delta Conformation (Partial Loop Insertion)		
1QMN	chymotrypsin inhibitor	460	e-129
1313184C	alpha-1-antichymotrypsin, precursor; alpha-1-antichymotrypsin	441	e-123
NP_001076.1	antichymotryp	439	e-123
sin	alpha-1-antichymotrypsin	439	e-123
2ACH	Chain A, Alpha1 Antichymotrypsin	434	e-121
NIM_011518			
NP_035648			
.1	Mrm.4708 U:+2.02	1198	0
NP_003168.2	spleen tyrosine kinase	1198	0
P43405	KSYK_HUMAN Tyrosine-protein kinase SYK (Spleen tyrosine kinase)	1198	0
A53596	protein-tyrosine kinase (EC 2.7.1.112) syk	1198	0
AAA36526.1	protein tyrosine kinase	1198	0
AAH02962.1	Similar to spleen tyrosine kinase	1198	0
AAH01645.1	Similar to spleen tyrosine kinase	1198	0
1918215A	protein Tyr kinase	1197	0
CAA51970.1	protein tyrosin kinase	1191	0
CAA82737.1	protein-tyrosine kinas	1140	0
AAH11399.1	Similar to spleen tyrosine kinase	1140	0
	similar to Tyrosine-protein kinase ZAP-70 (70 kDa zeta-associated protein)		
XP_047776.3	(Syk-related tyrosine kinase)	679	0
	ZA70_HUMAN Tyrosine-protein kinase ZAP-70 (70 kDa zeta-associated protein)		
P43403	(Syk-related tyrosine kinase)	679	0
A44266	protein-tyrosine kinase (EC 2.7.1.112) ZAP-70	677	0
2101280A	p72syk protein	658	0
AAH39039.1	Similar to zeta-chain (TCR) associated protein kinase (70kD)	519	e-146

NM_011236	1A81	A Chain A, Crystal Structure Of The Tandem Sh2 Domain Of The Syk Kinase Bound To A Dually Tyrosine-Phosphorylated Itam	498 e-140
	1A81	C Chain C, Crystal Structure Of The Tandem Sh2 Domain Of The Syk Kinase Bound To A Dually Tyrosine-Phosphorylated Itam	498 e-140
	1A81	E Chain E, Crystal Structure Of The Tandem Sh2 Domain Of The Syk Kinase Bound To A Dually Tyrosine-Phosphorylated Itam	498 e-140
	1A81	G Chain G, Crystal Structure Of The Tandem Sh2 Domain Of The Syk Kinase Bound To A Dually Tyrosine-Phosphorylated Itam	498 e-140
	1A81	I Chain I, Crystal Structure Of The Tandem Sh2 Domain Of The Syk Kinase Bound To A Dually Tyrosine-Phosphorylated Itam	498 e-140
	1A81	K Chain K, Crystal Structure Of The Tandem Sh2 Domain Of The Syk Kinase Bound To A Dually Tyrosine-Phosphorylated Itam	498 e-140
	BAC43747.1	truncated ZAP kinase	384 e-106
NP_035366		AD52 homolog isoform alpha; recombination protein RAD52; DNA repair protein RAD52	505 e-143
	NP_002870.2	RAD52	505 e-143
	P43351	RA52_HUMAN DNA repair protein RAD52 homolog	505 e-143
	AAB05203.1	homologue of yeast DNA repair and recombination enzyme (RAD52) gene	505 e-143
	AAA85793.1	RAD52	505 e-143
	AAA87554.1	recombination protein RAD52	503 e-142
	A57518	DNA repair protein RAD52	503 e-142
	1KN0	A Chain A, Crystal Structure Of The Human Rad52 Protein	384 e-106
	1KN0	B Chain B, Crystal Structure Of The Human Rad52 Protein	384 e-106
	1KN0	C Chain C, Crystal Structure Of The Human Rad52 Protein	384 e-106
	1KN0	D Chain D, Crystal Structure Of The Human Rad52 Protein	384 e-106
	1KN0	E Chain E, Crystal Structure Of The Human Rad52 Protein	384 e-106
	1KN0	F Chain F, Crystal Structure Of The Human Rad52 Protein	384 e-106
	1KN0	G Chain G, Crystal Structure Of The Human Rad52 Protein	384 e-106

1KN0	H Chain H, Crystal Structure Of The Human Rad52 Protein	384 e-106
1KN0	I Chain I, Crystal Structure Of The Human Rad52 Protein	384 e-106
1KN0	J Chain J, Crystal Structure Of The Human Rad52 Protein	384 e-106
1KN0	Chain K, Crystal Structure Of The Human Rad52	384 e-106
1H2I	A Chain A, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	B Chain B, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	C Chain C, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	D Chain D, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	E Chain E, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	F Chain F, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	G Chain G, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	H Chain H, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	I Chain I, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	J Chain J, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	K Chain K, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	L Chain L, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	M Chain M, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	N Chain N, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	O Chain O, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	P Chain P, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	Q Chain Q, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	R Chain R, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	S Chain S, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	T Chain T, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	U Chain U, Human Rad52 Protein, N-Terminal Domain	382 e-106
1H2I	V Chain V, Human Rad52 Protein, N-Terminal Domain	382 e-106
	RAD52 homolog isoform beta; recombination protein RAD52; DNA repair protein	5.000e
NP_602296.1	RAD52	283 -76
		5.000e
AAD24577.1	AF125950_1 DNA repair protein RAD52 beta Isoform	283 -76

Accession	Gene	Protein	Length	Score
NIP_011569	NP_602295.1	RAD52	207	-53
	AAD24576.1	AF125949_1 DNA repair protein RAD52 gamma isoform	207	-53
NIP_035699	NP_444515.1	tektin 1	683	0
	Q969V4	TEK1_HUMAN Tektin 1	683	0
	AAH14599.1	Similar to tektin 1	683	0
	AAL27695.1	AF357879_1 tektin protein	683	0
NIP_035699	NP_114104.1	tektin 3; testicular microtubules-related protein	291	-78
	Q9BXF9	TEK3_HUMAN Tektin 3	291	-78
	AAK15340.1	AF334676_1 testicular microtubules-related protein TEK3	291	-78
	BAB71464.1	unnamed protein product	290	-78
NIP_035699	AAH31688.1	tektin 3	289	-78
	NP_653306.1	hypothetical protein MGC27019	273	-73
	AAH21716.1	Similar to RIKEN cDNA 1700010L19 gene	273	-73
	NP_653275.1	hypothetical protein FLJ32871	267	-71

						3.000e
BAB71484.1	unnamed protein product					267 -71
						5.000e
NP_055281.2	tektin 2; testicular tektin B1-like protein					219 -57
						5.000e
Q9UIF3	TEK2_HUMAN Tektin 2 (Tektin-t) (Testicular tektin B1-like protein)					219 -57
						5.000e
BAA89350.1	h-TEKTIN-t					219 -57
						5.000e
CAC21454.1	dJ665N4.3 (novel tektin)					219 -57
						5.000e
AAH35620.1	tektin 2 (testicular)					219 -57
						2.000e
AAC09343.1	testicular tektin B1-like protein					218 -56
NIM_009349						
2104179A	Mm.299	U:+2.01				271 1e-072
AAD04723.1	unknown					
	Indolethylamine N-methyltransferase (Aromatic alkylamine N-methyltransferase)					
	(Indolamine N-methyltransferase) (Arylamine N-methyltransferase) (Amine					
O95050	N-methyltransferase)					267 2e-071
AAF18304.1	indolethylamine N-methyltransferase					267 2e-071
AAF18306.1	indolethylamine N-methyltransferase					267 2e-071
AAH33813.1	Unknown (protein for IMAGE:5209218)					266 5e-071
NP_006765.3	indolethylamine N-methyltransferase; thioester S-methyltransferase-like					266 5e-071
AAF18305.1	indolethylamine N-methyltransferase					266 5e-071
NP_006160.1	nicotinamide N-methyltransferase					239 7e-063
P40261	Nicotinamide N-methyltransferase					239 7e-063
A54060	nicotinamide N-methyltransferase (EC 2.1.1.1) - human					239 7e-063
AAA19904.1	nicotinamide N-methyltransferase					239 7e-063

NM_008757	AAA93158.1			nicotinamide N-methyltransferase	239	7e-063
	AAH00234.1			nicotinamide N-methyltransferase	239	7e-063
				outer dense fiber of sperm tails 1; outer dense fiber of sperm tails, 27-kD; outer		
				dense fibre of sperm tails 1	313	4e-085
I48699	NP_077721.1			Outer dense fiber protein	313	4e-085
	Q14990			outer dense fiber protein 2 - human	313	4e-085
	S71522			outer dense fiber protein	313	4e-085
	CAA52685.1			outer dense fiber protein	313	4e-085
NM_025746						
NP_080022						
.1	Mm.46142	U: +2	AAH14522.2	AAH14522.2	206	1e-052
			XP_370630.1	protein phosphatase 1, regulatory (inhibitor) subunit 14B	206	1e-052
			2208307A	PNG gene	206	1e-052
NM_007702	Mm.449	U: +1.88	AAC34987.1	cell death activator CIDE-A		
NP_031728.						
1						
			AAH31896.1	Similar to cell death-inducing DFFA-like effector a	340	3.00e-92
					319	5.00e-86

MASTER TABLE 1: Subtable 1C Mixed Genes/Proteins

Mouse Gene	Human	Protein	Behavior	Unigene	Human Protein Name	Score (bits)	E-value
AA103180			U: +20.78				
CAA09617.1	Mm.16773	F:27.76		AAH39235.1	similar to albumin	276	1.00e-74
		1BKE			Human Serum Albumin In A Complex With Myristic Acid And Tri-Iodobenzoic Acid	276	1.00e-74
		1AO6			A Chain A, Crystal Structure Of Human Serum Albumin	276	1.00e-74
		1AO6			B Chain B, Crystal Structure Of Human Serum Albumin	276	1.00e-74
					X-Ray Study Of Recombinant Human Serum Albumin. Phases Determined By		
					Molecular Replacement Method, Using Low Resolution Structure Model Of		
		1UOR			Tetragonal Form Of Human Serum Albumin	276	1.00e-74
		1BJ5			Human Serum Albumin Complexed With Myristic Acid	276	1.00e-74
		1BM0			A Chain A, Crystal Structure Of Human Serum Albumin	276	1.00e-74
		1BM0			B Chain B, Crystal Structure Of Human Serum Albumin	276	1.00e-74
		1E7E			A Chain A, Human Serum Albumin Complexed With Decanoic Acid (Capric Acid)	276	1.00e-74
		1E7F			A Chain A, Human Serum Albumin Complexed With Dodecanoic Acid (Lauric Acid)	276	1.00e-74
					A Chain A, Human Serum Albumin Complexed With Tetradecanoic Acid (Myristic		
		1E7G			Acid) Human Serum Albumin Complexed With Myristic Acid	276	1.00e-74
					A Chain A, Human Serum Albumin Complexed With Octadecanoic Acid (Stearic		
		1E7I			Acid)	276	1.00e-74
					A Chain A, Human Serum Albumin Complexed With Hexadecanoic Acid (Palmitic		
		1E7H			Acid)	276	1.00e-74
					A Chain A, Crystal Structure Of Human Serum Albumin Complexed With The		
		1E7A			General Anesthetic Propofol	276	1.00e-74
					B Chain B, Crystal Structure Of Human Serum Albumin Complexed With The		
		1E7A			General Anesthetic Propofol	276	1.00e-74
					A Chain A, Crystal Structure Of Human Serum Albumin Complexed With The		
		1E7B			General Anesthetic Halothane	276	1.00e-74

1E7B	B Chain B, Crystal Structure Of Human Serum Albumin Complexed With The General Anesthetic Halothane	276 1.00e-74
1E7C	A Chain A, Human Serum Albumin Complexed With Myristic Acid And The General Anesthetic Halothane	276 1.00e-74
1E78	A Chain A, Crystal Structure Of Human Serum Albumin	276 1.00e-74
1E78	B Chain B, Crystal Structure Of Human Serum Albumin	276 1.00e-74
1H9Z	A Chain A, Human Serum Albumin Complexed With Myristic Acid And The R-(+) Enantiomer Of Warfarin	276 1.00e-74
1HA2	A Chain A, Human Serum Albumin Complexed With Myristic Acid And The S-(-) Enantiomer Of Warfarin	276 1.00e-74
1GNI	A Chain A, Human Serum Albumin Complexed With Cis-9-Octadecenoic Acid (Oleic Acid)	276 1.00e-74
1GNJ	Cis-5,8,11,14-Eicosatetraenoic Acid (Arachidonic Acid) similar to human albumin, Swiss-Prot Accession Number P02768; Method:	276 1.00e-74
AAA64922.1	conceptual translation supplied by author	276 1.00e-74
AAA98798.1	alloalbumin Venezia	276 1.00e-74
AAF01333.1	AF190168_1 serum albumin precursor	276 1.00e-74
CAA23753.1	reading frame HSA	276 1.00e-74
CAA23754.1	serum albumin	276 1.00e-74
AAN17825.1	serum albumin	276 1.00e-74
NP_000468.1	albumin precursor; PRO0883 protein	276 1.00e-74
P02768	ALBU_HUMAN Serum albumin precursor	276 1.00e-74
ABHUS	serum albumin precursor	276 1.00e-74
AAA98797.1	albumin	276 1.00e-74
AAF69594.1	AF119917_2 PRO0903	276 1.00e-74
AAH34023.1	albumin	276 1.00e-74
AAH36003.1	similar to serum albumin	276 1.00e-74

[illegible]

A1AT_HUMAN Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor)			
P01009	(Alpha-1-antitrypsin precursor)		519 e-147
ITHU	alpha-1-antitrypsin precursor		519 e-147
CAA25838.1	alpha 1-antitrypsin		519 e-147
AAB59375.1	alpha-1-antitrypsin		519 e-147
AAG35496.1	AF130117_27 PRO2209		519 e-147
CAD61914.1	unnamed protein product		519 e-147
CAD62306.1	unnamed protein produc		519 e-147
AAA51547.1	alpha-1-antitrypsin precursor		519 e-147
	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase,		
NP_000286.	antitrypsin), member 1; Protease inhibitor (alpha-1-antitrypsin); protease inhibitor 1		
2	(anti-elastase), alpha-1-antitrypsin	518	e-147
	Similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase,		
AAH11991.1	antitrypsin), member 1	518	e-147
AAF29581.1	AF113676_1 PRO0684	516	e-146
AAB59495.1	alpha-1-antitrypsin	516	e-146
AAA51546.1	alpha-1-antitrypsin	513	e-145
	A Chain A, A 2.1 Angstrom Structure Of An Uncleaved Alpha-1-Antitrypsin Shows		
1HP7	Variability Of The Reactive Center And Other Loops	511	e-144
1KCT	Alpha1-Antitrypsin	510	e-144
NM_017399			
NP_059095.			
1	U:+10.38 NP_001434.		
	Mm.22126 F:12.18		
P07148	fatty acid binding protein 1, liver; Fatty acid-binding protein, liver; L-FABP	215	2.00e-56
FZHUL	FABL_HUMAN Fatty acid-binding protein, liver (L-FABP)	215	2.00e-56
AAA52419.1	fatty acid-binding protein, hepatic	215	2.00e-56
AAH32801.1	L-FABP	215	2.00e-56
AAA52418.1	fatty acid binding protein 1, liver	215	2.00e-56
	fatty acid binding protein	213	7.00e-56

AK011118

1FZG	B Chain B, Crystal Structure Of Fragment D From Human Fibrinogen With The			
	Peptide Ligand Gly-His-Arg-Pro-Amide		489	e-138
	E Chain E, Crystal Structure Of Fragment D From Human Fibrinogen With The			
	Peptide Ligand Gly-His-Arg-Pro-Amide		489	e-138
1FZG	B Chain B, Crystal Structure Of Human D-Dimer From Cross-Linked Fibrin			
	Complexed With Gpr And Ghrpldk Peptide Ligands.		489	e-138
	E Chain E, Crystal Structure Of Human D-Dimer From Cross-Linked Fibrin			
	Complexed With Gpr And Ghrpldk Peptide Ligands.		489	e-138
1N86	B Chain B, Fragment Double-D From Human Fibrin		489	e-138
	E Chain E, Fragment Double-D From Human Fibrin		489	e-138
	NP_068656.			
	1	fibrinogen, gamma chain isoform gamma-B precursor	184	9.00e-56
AAB59530.1	fibrinogen gamma-prime chain		184	9.00e-56
	NP_000500.			
	1	fibrinogen, gamma chain isoform gamma-A precursor	184	9.00e-56
	AAB59531.1	fibrinogen gamma chain	184	9.00e-56
P02679	FIBG_HUMAN Fibrinogen gamma chain precursor (PRO2061)		184	4.00e-55
	FGHUGB fibrinogen gamma-B chain precursor		184	4.00e-55
	AAK19752.2 AF350254_2 fibrinogen gamma chain, isoform gamma-B precursor		184	4.00e-55
	FGHUG	fibrinogen gamma-A chain precursor	184	4.00e-55
AAF22036.1	AF118094_31 PRO2061		184	4.00e-55
	AAH07044.1 fibrinogen, gamma polypeptide		184	4.00e-55
	AAK19751.2 AF350254_1 fibrinogen gamma chain, isoform gamma-A precursor		184	4.00e-55
	AAH21674.1	fibrinogen, gamma polypeptide	184	4.00e-55
NM_009244				
NP_033270.				
1	U:+6.8			
	Mm.193418	F:6.19	508	e-144
	alpha-1-antitrypsin precursor			
	Similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase,			
AAH15642.1	antitrypsin), member 1		508	e-144

1012287A	antitrypsin alpha1 mutant	507	e-143
	A1AT_HUMAN Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor)		
P01009	(Alpha-1-antitrypsinase) (PRO0684/PRO2209)	507	e-143
ITHU	alpha-1-antitrypsin precursor	507	e-143
CAA25838.1	alpha 1-antitrypsin	507	e-143
AAB59375.1	alpha-1-antitrypsin	507	e-143
AAG35496.1	AF130117_27 PRO2209	507	e-143
CAD61914.1	unnamed protein product	507	e-143
CAD62306.1	unnamed protein product	507	e-143
	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antitrypsinase,		
NP_000286.	antitrypsin), member 1; Protease inhibitor (alpha-1-antitrypsin); protease inhibitor 1		
2	(anti-elastase), alpha-1-antitrypsin	506	e-143
	Similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antitrypsinase,		
AAH11991.1	antitrypsin); member 1	506	e-143
AAF29581.1	AF113676_1 PRO0684	504	e-142
AAB59495.1	alpha-1-antitrypsin	504	e-142
AAA51546.1	alpha-1-antitrypsin	501	e-141
	A Chain A, A 2.1 Angstrom Structure Of An Uncleaved Alpha-1-Antitrypsin Shows		
1HP7	Variability Of The Reactive Center And Other Loops	499	e-141
1KCT	Alpha1-Antitrypsin	498	e-141
NP_005243.	v-fos FBJ murine osteosarcoma viral oncogene homolog; FBJ murine		
1	osteosarcoma viral (v-fos) oncogene homolog (oncogene FOS)	557	e-158
	FOS_HUMAN Proto-oncogene protein c-fos (Cellular oncogene fos) (G0/G1 switch		
P01100	regulatory protein 7)	557	e-158
TVHUF1	transforming protein fos - human	557	e-158
CAA24756.1	c-fos	557	e-158
AAA52471.1	c-fos protein	557	e-158
AAC98315.1	cfos	557	e-158
AAH04490.1	V-fos FBJ murine osteosarcoma viral oncogene homolog	557	e-158
AAO21129.1	v-fos FBJ murine osteosarcoma viral oncogene homolog	557	e-158

NM_009393	BAA87921.1	cellular oncogene c-fos	306	9e-083
NP_033419.	NP_003271.			
1	U:+4.67	troponin C, slow; Troponin-C1, slow; troponin C1, slow; cardiac troponin C	300	9.00e-82
	F:2.15	troponin C, cardiac and slow skeletal muscle	300	9.00e-82
	Mm.712	troponin C (AA 1-161)	300	9.00e-82
		CAA30736.1	300	9.00e-82
		AAA36772.1	300	9.00e-82
		slow twitch skeletal/cardiac muscle troponin C	300	9.00e-82
		AAH30244.1	300	9.00e-82
		troponin C, slow	300	9.00e-82
		P02590	299	3.00e-81
		TPCC_HUMAN Troponin C, slow skeletal and cardiac muscles (TN-C)	294	9.00e-80
NM_007729	AAB91994.1	cardiac ventricular troponin C		
NP_031755.				
1	U:+4.03	collagen type XI alpha-1 isoform A	709	0
	F:14.03	AAF04725.1		
	Mm.5017	NP_001845.		
		2		
		alpha 1 type XI collagen isoform A preproprotein; collagen XI, alpha-1 polypeptide	709	0
		P12107	709	0
		CA1B_HUMAN Collagen alpha 1(XI) chain precursor		
		CGHU1E	709	0
		collagen alpha 1(XI) chain precursor		
		AAA51891.1	709	0
		alpha-1 (type XI) collagen precursor		
		NP_542196.		
		1		
		alpha 1 type XI collagen isoform B preproprotein; collagen XI, alpha-1 polypeptide	669	0
		AAF04724.1	665	0
		collagen type XI alpha-1		
		NP_542197.		
		1		
		alpha 1 type XI collagen isoform C preproprotein; collagen XI, alpha-1 polypeptide	665	0
		NP_000084.		
		2		
		alpha 1 type V collagen preproprotein	476	e-133
	U:+3.91	J569D19.1 (similar to mouse Ras, Dexamethasone-induced 1		
AK015898				
NP_033052	Mm.179267	CAA18456.1	517	e-146
	F:4.02	(Ras-related protein, RASD1, DEXRAS1))		
		AAG00868.1	517	e-146
		tumor endothelial marker 2		

NP_055125.2	RASD family, member 2; tumor endothelial marker 2; Ras homolog enriched in striatum; GTP-binding protein Rhes	510	e-144
Q96D21	GTP-binding protein Rhes (Ras homolog enriched in striatum) (Tumor endothelial marker 2)	510	e-144
AAH13419.1	RASD family, member 2	510	e-144
NP_057168.1	RAS, dexamethasone-induced 1; ras-related protein; dexamethasone-induced ras-related protein 1; activator of G protein signaling	335	1e-091
Q9Y272	Dexamethasone-induced Ras-related protein 1 (Activator of G-protein signaling 1)	335	1e-091
AAD34206.1	activator of G protein signaling	335	1e-091
AAD34621.1	ras-related protein	335	1e-091
AAF01364.1	ras-related protein	335	1e-091
AAG44256.1	activator of G-protein signaling; AGS1	335	1e-091
AAH18041.1	RAS, dexamethasone-induced 1	335	1e-091
AAM21071.1	activator of G protein signaling	335	1e-091
AAF72997.1	dexamethasone-induced ras-related protein 1	335	1e-091
AAG17979.1	unknown	209	8e-054
NM_021462	U:+3.6		
NP_951009.1	MAP kinase-interacting serine/threonine kinase 2; G protein-coupled receptor kinase 7	798	0
AAG26336.1	MAP kinase-interacting kinase 2a	798	0
AAD21217.1	Putative map kinase interacting kinase	798	0
Q9HBH9	MAP kinase-interacting serine/threonine kinase 2 (MAP kinase signal-integrating kinase 2) (Mnk2)	775	0
NP_060042.2	MAP kinase-interacting serine/threonine kinase 2; G protein-coupled receptor kinase 7	679	0
AAG26337.1	MAP kinase-interacting kinase 2b	679	0
AAF17226.1	map kinase-interacting kinase	678	0
BAA19885.1	MNK1	585	e-166
T46505	hypothetical protein DKFZp586A1021.1 - human (fragment)	582	e-165

[illegible]

1KV3 C	Chain C, Human Tissue Transglutaminase In Gdp Bound Form	1188	0
1KV3 D	Chain D, Human Tissue Transglutaminase In Gdp Bound Form	1188	0
1KV3 E	Chain E, Human Tissue Transglutaminase In Gdp Bound Form	1188	0
1KV3 F	Chain F, Human Tissue Transglutaminase In Gdp Bound Form	1188	0
NP_945189.1	transglutaminase 2 isoform b; transglutaminase C; tissue		
1	transglutaminase; TGase C; TGase-H		
AAH03551.1	Transglutaminase 2, isoform b	968	0
	protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) 2, splice	968	0
A44302	form 2 - human		
AAA36739.1	transglutaminase	966	0
AAF23981.1	transglutaminase X	966	0
	Protein-glutamine gamma-glutamyltransferase X (TGase X) (TGX) (TG(X))	559	e-158
O43548	(Transglutaminase 5)		
AAC02978.1	transglutaminase X	557	e-158
NP_443187.1		554	e-157
1	transglutaminase Z		
	Protein-glutamine gamma-glutamyltransferase Z (TGase Z) (TGZ) (TG(Z))	533	e-151
Q96PF1	(Transglutaminase 7)		
AAK97573.1	transglutaminase Z	533	e-151
	Chain A, Three-Dimensional Structure Of The Human Transglutaminase 3	533	e-151
	Enzyme: Binding Of Calcium Ions Change Structure For		
pdb 1L9M A	Activation		
	Chain B, Three-Dimensional Structure Of The Human Transglutaminase 3	510	e-144
	Enzyme: Binding Of Calcium Ions Change Structure For		
pdb 1L9M B	Activation		
	Chain A, Three-Dimensional Structure Of The Human Transglutaminase 3	510	e-144
	Enzyme: Binding Of Calcium Ions Change Structure For		
pdb 1L9N A	Activation		
		510	e-144

Chain B, Three-Dimensional Structure Of The Human Transglutaminase 3			
Enzyme: Binding Of Calcium Ions Change Structure For Activation			
Chain A, Role Of Calcium Ions In The Activation And Activity Of The Transglutaminase 3 Enzyme (3 Calciums, Active Form)	510	e-144	510
Chain B, Role Of Calcium Ions In The Activation And Activity Of The Transglutaminase 3 Enzyme (3 Calciums, Active Form)	510	e-144	510
Chain A, Role Of Calcium Ions In The Activation And Activity Of The Transglutaminase 3 Enzyme	510	e-144	510
Chain A, Role Of Calcium Ions In The Activation And Activity Of The Transglutaminase 3 Enzyme (2 Calciums, 1 Mg, Inactive Form)	510	e-144	510
Chain B, Role Of Calcium Ions In The Activation And Activity Of The Transglutaminase 3 Enzyme (2 Calciums, 1 Mg, Inactive Form)	510	e-144	510
Chain A, Structural Basis For The Coordinated Regulation Of Transglutaminase 3 By Guanine Nucleotides And CalciumMAGNESIUM	510	e-144	510
Chain B, Structural Basis For The Coordinated Regulation Of Transglutaminase 3 By Guanine Nucleotides And CalciumMAGNESIUM	510	e-144	510
Chain A, Structural Basis For The Coordinated Regulation Of Transglutaminase 3 By Guanine Nucleotides And CalciumMAGNESIUM	510	e-144	510
Chain B, Structural Basis For The Coordinated Regulation Of Transglutaminase 3 By Guanine Nucleotides And CalciumMAGNESIUM	510	e-144	510

Accession	Gene	Protein	Function	Score	Length
NM_011814	U: +3.1	1	Fragile X mental retardation syndrome related protein 2	1012	0
NP_035944	F: 6.44	1	fragile X mental retardation, autosomal homolog 2	1012	0
	Mm.41930	1	fragile X mental retardation syndrome related protein 2	1010	0
		1	fragile X mental retardation syndrome related protein 2; fragile X-mental retardation		
		1	1-like 2	1009	0
		1	Fragile X mental retardation syndrome related protein 2	1009	0
		1	fragile X mental retardation syndrome related protein FXR2 - human	1009	0
		1	fragile X mental retardation syndrome related protein	1009	0
		1	fragile X mental retardation-related protein 1; Fragile X mental retardation,		
		1	autosomal homolog	635	0
		1	Fragile X mental retardation syndrome related protein 1	635	0
		1	fragile X mental retardation syndrome related protein FXR1 - human	635	0
		1	FXR1	635	0
		1	FXR1 protein	613	e-175
		1	FMR1	510	e-144
		1	fragile X mental retardation autosomal homolog 1-like protein	494	e-139
		1	fragile X mental retardation syndrome protein	464	e-130
		1	fragile X mental retardation syndrome protein	464	e-130
		1	fragile X mental retardation syndrome protein	464	e-130
NM_025285					
NP_079561	U: +2.90	1	Similar to superiorcervical ganglia, neural specific 10	345	2.00e-94
	F: 5.69	1	superiorcervical ganglia, neural specific 10; neuronal growth-associated protein		
	Mm.29580	1	(silencer element); superior cervical ganglia, neural specific 10	342	1.00e-93
		1	SCG10	342	1.00e-93
		1	STN2_HUMAN Stathmin 2 (SCG10 protein) (Superior cervical ganglion-10 protein)	342	1.00e-93

BAA23326.1	silencer element	342	1.00e-93
NP_056978.			
2	SCG10-like-protein	249	1.00e-65
Q9NZ72	STN3_HUMAN Stathmin 3 (SCG10-like protein)	249	1.00e-65
AAF35245.1	SCG10 like-protein	249	1.00e-65
	bK3184A7.2 (SCG10-like protein (SCLIP) (ortholog of rabbit neuroplasticin-2		
CAC16222.1	(NPC2)))	249	1.00e-65
AAH09381.1	Unknown (protein for MGC:16668)	249	1.00e-65
AAD12730.1	SCG10-like-protein	248	2.00e-65
BAC11252.1	unnamed protein product	245	2.00e-64
Q9H169	STN4_HUMAN Stathmin 4 (Stathmin-like protein B3) (RB3)	217	5.00e-56
CAC22254.1	RB3 protein	217	5.00e-56
CAB66503.1	hypothetical protein	217	5.00e-56
NP_110422.			
2	stathmin-like-protein RB3	206	7.00e-53
AAH11520.1	Similar to stathmin-like-protein RB3	206	7.00e-53
NP_054798.	Kruppel-like factor 15; KKLf protein; kidney-enriched Kruppel-like		
1	factor	624	e-178
Q9UIH9	Kruppel-like factor 15 (Kidney-enriched kruppel-like factor)	624	e-178
BAA88561.1	KKLF	624	e-178
AAH36733.1	Kruppel-like factor 15	624	e-178
XP_351115.			
AK012059			
S48861			
1	similar to KIAA0100 protein	594	e-170
XP_371036.			
1	KIAA0100 gene product	594	e-170
BAA07891.2	KIAA0100 protein	594	e-170
S74567			
U:+2.84			
AAO16209.1	c-maf proto-oncogene	416	e-116
N/A			
AAC27037.1	short form transcription factor C-MAF	230	1e-059

				v-maf musculoaponeurotic fibrosarcoma oncogene homolog; Avian				
				NP_005351.	musculoaponeurotic fibrosarcoma (MAF) protooncogene; v-maf			
				2	musculoaponeurotic fibrosarcoma (avian) oncogene homolog			
				O75444	Transcription factor Maf (Proto-oncogene c-maf)			
				AAC27038.1	long form transcription factor C-MAF			
NM_011930			U:-2.84	NP_001278.				
O70496		Mm.270587	F:4	1	chloride channel 7; ClC-7	1395	0	3e-059
				P51798	Chloride channel protein 7 (ClC-7)	1395	0	3e-059
				AAF34711.1	chloride channel protein 7	1395	0	3e-059
				AAH12737.1	Chloride channel 7	1395	0	3e-059
				AAK61282.1	putative chloride channel protein 7	1388	0	3e-059
				S68427	chloride channel protein 7 (ClC-7) - human (fragment)	1359	0	3e-059
				CAA91556.1	CLC-7 chloride channel protein	1359	0	3e-059
				AAH06158.1	CLCN7 protein	864	0	3e-059
				AAH04946.1	Unknown (protein for IMAGE:3615790)	499	0	3e-059
				BAA05836.4	KIAA0046	447	0	3e-059
				NP_001277.				
				1	chloride channel 6 isoform ClC-6a	447	0	3e-059
				P51797	Chloride channel protein 6 (ClC-6)	447	0	3e-059
				S68428	probable chloride channel ClC-6 - human	447	0	3e-059
				CAA58292.1	putative chloride channel	447	0	3e-059
				AAB69287.1	putative chloride channel	447	0	3e-059
				CAA15951.1	dJ934G17.1.1 (chloride channel protein ClC-6A (KIAA0046))	442	0	3e-059
				CAA67836.1	chloride channel	257	0	3e-059
				CAA05083.1	ClC-7 chloride channel	250	0	3e-059
NM_016906			U:-2.79	NP_037468.	Sec61 alpha form 1; sec61 homolog; protein transport protein SEC61			
P38378		Mm.28375	F:3.89	1	alpha subunit isoform 1	931	0	3e-059
					Protein transport protein Sec61 alpha subunit isoform 1 (Sec61			
				P38378	alpha-1)	931	0	3e-059

AAD39847.1	sec61 homolog			931	0
AAK29083.1	Sec61 alpha form 1			931	0
	Protein transport protein Sec61 alpha subunit isoform 2 (Sec61 alpha-2)				
Q9Y2R3				909	0
AAD27765.1	sec61 homolog			909	0
NP_060614.2	Sec61 alpha form 2			891	0
AAK29084.1	Sec61 alpha form 2			891	0
AAH02951.1	SEC61A1 protein			828	0
AAH26179.1	SEC61A2 protein			778	0
BAB14148.1	unnamed protein product			775	0
BAC11298.1	unnamed protein product			696	0
BAA91692.1	unnamed protein product			432	e-120
BAB13955.1	unnamed protein product			432	e-120
CAD38592.1	hypothetical protein			425	e-118
BAC11283.1	unnamed protein product			338	3e-092
BAC11434.1	unnamed protein product			338	3e-092
NP_004753.1	pleckstrin homology, Sec7 and coiled/coil domains 1 isoform 1; homolog of secretory protein SEC7; cytoadhesin 1			802	0
U:2.73					
F:5.98					
NM_011180					
Q9QX11	Mm.86413			802	0
	Cytohesin 1 (SEC7 homolog B2-1)			802	0
S24168	SEC7 homolog - human			802	0
AAA36602.1	yeast sec7 gene homologue			802	0
AAH50452.1	Pleckstrin homology, Sec7 and coiled/coil domains 1, isoform 1			802	0
NP_059430.1	pleckstrin homology, Sec7 and coiled/coil domains 1 isoform 2; homolog of secretory protein SEC7; cytoadhesin 1			773	0
AAF37738.1	cytohesin 1			765	0
AAF37737.1	cytohesin 1			758	0
NP_059431.1	pleckstrin homology, Sec7 and coiled/coil domains 2 isoform 1; pleckstrin homology, Sec7 and coiled/coil domains 2; cytohesin 2			689	0

	Cytohesin 2 (ARF nucleotide-binding site opener) (ARNO protein) (ARF exchange factor)				689	0
	AAB09591.1 cytohesin-2				689	0
	AAH04361.1 Pleckstrin homology, Sec7 and coiled/coil domains 2, isoform 1				689	0
	AAH38713.1 Pleckstrin homology, Sec7 and coiled/coil domains 2, isoform 1				687	0
	Cytohesin 3 (ARF nucleotide-binding site opener 3) (ARNO3 protein) (General receptor of phosphoinositides 1) (Grp1)				684	0
	O43739 pleckstrin homology, Sec7 and coiled/coil domains 2 isoform 2; pleckstrin homology, Sec7 and coiled/coil domains 2; pleckstrin homology, Sec7 and coiled/coil domains 2; pleckstrin homology, Sec7 and coiled/coil domains 2; pleckstrin homology, Sec7 and coiled/coil domains 2;					
	NP_004219.1 coiled/coil domains 2;				682	0
	CAA68084.1 Arno protein (ARF exchange factor)				682	0
	NP_004218.1 pleckstrin homology, Sec7 and coiled/coil domains 3; cytohesin 3; ARF nucleotide-binding site opener 3; general receptor of phosphoinositides 1				677	0
	1 CAA11686.1 ARNO3				677	0
	CAA06434.1 GRP1 protein				677	0
	AAH28717.1 Pleckstrin homology, Sec7 and coiled/coil domains 3				677	0
	AAS00357.1 unknown				676	0
NM_025583						
NP_079859.	U:+2.6					
1	Mm.34374	F:2.03				
	NP_001897.					
	1 chymotrypsinogen B1				479	e-135
	P17538 CTB_HUMAN Chymotrypsinogen B precursor				479	e-135
	A31299 chymotrypsin (EC 3.4.21.1) precursor				479	e-135
	AAA52128.1 preprochymotrypsinogen (EC 3.4.21.1)				479	e-135
	AAH05385.1 chymotrypsinogen B1				479	e-135
	AAH39716.1 Similar to chymotrypsin-like				305	7.00e-83
	NP_001898.					
	1 chymotrypsin-like; Chymotrypsin-like protease				302	5.00e-82
	P40313 CTRL HUMAN Chymotrypsin-like protease CTRL-1 precursor				302	5.00e-82

138136	chymotrypsin-like proteinase (EC 3.4.21.-) CTRL-1				302	5.00e-82
CAA50710.1	chymotrypsin-like protease CTRL-1				302	5.00e-82
CAA50711.1	chymotrypsin-like protease CTRL-1				302	5.00e-82
NP_031378.1	elastase 3B				197	2.00e-50
B29934	pancreatic elastase (EC 3.4.21.36) IIIB precursor				197	2.00e-50
AAA58454.1	elastase III B				197	2.00e-50
P08861	EL3B_HUMAN Elastase IIIB precursor (Protease E)				196	3.00e-50
AAH05216.1	elastase 3B				196	3.00e-50
Q99895	CLCR_HUMAN Caldecrin precursor (Chymotrypsin C)				195	6.00e-50
S68825	pancreatic elastase (EC 3.4.21.36) isoform 1 precursor				195	6.00e-50
CAC42420.1	bA265F14.1 (chymotrypsin C (caldecrin))				195	6.00e-50
AAH15118.1	chymotrypsin C (caldecrin)				195	6.00e-50
NM_023764						
NP_076253.1						
U: +2.56						
Mm.103551						
F:3.93						
CAB66769.1	hypothetical protein				431	e-120
AAH04420.1	TOLLIP protein				431	e-120
AAH12057.1	TOLLIP protein				431	e-120
AAH18272.1	TOLLIP protein				431	e-120
CAB58118.1	TOLLIP protein				426	e-118
BAB14283.1	unnamed protein product				339	2e-092
BAC04844.1	unnamed protein product				223	2e-057
NP_002220.1						
U: +2.54						
Mm.1167						
F:3.12						
1	jun B proto-oncogene				518	e-146
P17275	Transcription factor jun-B				518	e-146
TVHUJB	transforming protein jun-B - human				518	e-146
CAA35738.1	unnamed protein product				518	e-146
AAA59198.1	transactivator				518	e-146
AAA74915.1	transcription factor junB				518	e-146
NM_008416						
P09450						

AAH04250.1	Jun B proto-oncogene	518	e-146
AAH09466.1	Jun B proto-oncogene	518	e-146
AAH09465.1	Jun B proto-oncogene	517	e-146
1404381A	c-jun oncogene	215	2e-055
	v-jun avian sarcoma virus 17 oncogene homolog; Jun activation domain		
NP_002219.	binding protein; activator protein 1; enhancer-binding		
1	protein AP1	215	2e-055
	Transcription factor AP-1 (Activator protein 1) (AP1) (Proto-oncogene		
	c-jun) (V-jun avian sarcoma virus 17 oncogene homolog)		
P05412	(p39)	215	2e-055
AAA59197.1	JUN	215	2e-055
	bA63G10.1 (transcription factor AP-1 (proto-oncogen C-Jun) (P39)		
CAC10201.1	(GOS7))	215	2e-055
AAH06175.1	V-jun avian sarcoma virus 17 oncogene homolog	215	2e-055
AAO22993.1	v-jun sarcoma virus 17 oncogene homolog (avian)	215	2e-055
TVHUJN	transcription factor AP-1 - human	214	3e-055
NP_005345.			
2	jun D proto-oncogene; transcription factor jun-D; JunD-FL isoform	202	1e-051
P17535	JUND_HUMAN Transcription factor JUN-D	202	1e-051
A43815	transforming protein (jun-D) (version 2) - human	202	1e-051
CAA40010.1	junD protein	202	1e-051
AAH52571.1	Unknown (protein for MGC:59742)	200	6e-051
AK011195	U:+2.50		
XP_133445	Mm.276298		
	F:3.38	292	4e-079
	NP_079405.		
2	hypothetical protein FLJ22688	292	4e-079
AAH04445.1	hypothetical protein FLJ22688	292	4e-079
AAH16793.1	hypothetical protein FLJ22688	292	4e-079
AAH10092.1	FLJ22688 protein	214	9e-056

NM_029020
NP_062425.

Accession	Gene	Protein	Accession	Gene	Protein	Accession	Gene	Protein
NM_017376	NP_059072.1	1	U:2.41	NP_003207.1	thyrotrophic embryonic factor; thyrotroph embryonic factor	446	e-124	
			Mm.270278	G02360	thyrotroph embryonic factor - human	446	e-124	
				AAB06497.1	thyrotroph embryonic factor	446	e-124	
				AAH39258.1	Thyrotrophic embryonic factor	446	e-124	
				AAH42476.1	Thyrotrophic embryonic factor	446	e-124	
				Q10587	Thyrotroph embryonic factor	410	e-114	
				dJ979N1.5.1	(thyrotrophic embryonic factor (ortholog of chicken vitellogenin gene-binding protein VBP alpha/alpha variant) (variant 1))	410	e-114	
				AAA81373.1	thyrotroph embryonic factor	410	e-114	
				dJ979N1.5.2	(thyrotrophic embryonic factor (ortholog of chicken vitellogenin gene-binding protein VBP beta/beta variant) (variant 2))	403	e-111	
				CAB62497.1	hypothetical protein	278	5e-074	
				NP_002117.1				
				1	hepatic leukemia factor	259	3e-068	
				Q16534	Hepatic leukemia factor	259	3e-068	
				A44064	hepatic leukemia factor - human	259	3e-068	
				AAA52675.1	hepatic leukemia factor	259	3e-068	
				CAA48777.1	hepatic leukemia factor	259	3e-068	
				AAH36093.1	hepatic leukemia factor	259	3e-068	
				NP_001343.2	D site of albumin promoter (albumin D-box) binding protein; D site of albumin promoter binding protein	209	2e-053	
				Q10586	D-site-binding protein (Albumin D box-binding protein) (TAXREB302)	209	2e-053	
				AAB18668.1	D-site binding protein	209	2e-053	
				AAB50219.1	albumin D-box binding protein	209	2e-053	
				AAH11965.1	D site of albumin promoter (albumin D-box) binding protein	209	2e-053	

NIM_010092 NP_034222. 1	U:-2.36 F:4.8 Mm.57249	AAP35482.1	D site of albumin promoter (albumin D-box) binding protein	209	2e-053
		A55558	albumin D-box binding protein - human	209	2e-053
		AAA81374.1	albumin D-box binding protein	209	2e-053
NP_006474. 1	U:-2.36 F:4.8 Mm.57249	NP_006474.	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	874	0
		1	isoform b; minibrain-related kinase	874	0
		CAA76990.1	Dyrk1B protein kinase		
		NP_006475.	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	865	0
		1	isoform c; minibrain-related kinase	865	0
		CAA76989.1	Dyrk1B protein kinase		
		NP_004705.	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	855	0
		1	isoform a; minibrain-related kinase		
			Dual-specificity tyrosine-phosphorylation regulated kinase 1B (Mirk		
		Q9Y463	protein kinase) (Minibrain-related kinase)	855	0
		JG0195	protein kinase DYRK1B (EC 2.7.1.-) - human	855	0
		CAA76991.1	Dyrk1B protein kinase	855	0
		AAF15893.1	protein kinase MIRK	855	0
			Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B,		
		AAH18751.1	isoform a	855	0
NP_569120. 1	U:-2.36 F:4.8 Mm.57249	AAH25291.1	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B,	855	0
		AAC28914.1	isoform a	754	0
			dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A		
			isoform 2; minibrain (Drosophila) homolog; protein kinase		
			minibrain homolog; dual specificity YAK1-related kinase;		
NP_569120. 1	U:-2.36 F:4.8 Mm.57249		serine/threonine-specific protein kinase; mnb protein		
			kinase homolog hp86; serine/threonine kinase MNB; MNB		
			protein kinase; MNB/DYRK protein kinase	612	e-175

JC4898	Down-syndrome-critical-region protein - human	612	e-175
BAA12866.1	MNB protein kinase	612	e-175
BAA13110.1	serine/threonine protein kinase	612	e-175
	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A		
	isoform 1; minibrain (Drosophila) homolog; protein kinase		
	minibrain homolog; dual specificity YAK1-related kinase;		
	serine/threonine-specific protein kinase; mnb protein		
NP_001387.	kinase homolog hp86; serine/threonine kinase MNB; MNB	612	e-175
2	protein kinase; MNB/DYRK protein kinase		
	Dual-specificity tyrosine-phosphorylation regulated kinase 1A		
	(Protein kinase minibrain homolog) (MNBH) (HP86) (Dual		
	specificity YAK1-related kinase)		
Q13627		612	e-175
AAB18639.1	MNB	612	e-175
AAC50939.1	hp86	610	e-174
	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A		
	isoform 3; minibrain (Drosophila) homolog; protein kinase		
	minibrain homolog; dual specificity YAK1-related kinase;		
	serine/threonine-specific protein kinase; mnb protein		
NP_567824.	kinase homolog hp86; serine/threonine kinase MNB; MNB	608	e-173
1	protein kinase; MNB/DYRK protein kinase	608	e-173
AAD31169.1	serine-threonine protein kinase		
	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A		
	isoform 5; minibrain (Drosophila) homolog; protein kinase		
	minibrain homolog; dual specificity YAK1-related kinase;		
	serine/threonine-specific protein kinase; mnb protein		
NP_569122.	kinase homolog hp86; serine/threonine kinase MNB; MNB	603	e-172
1	protein kinase; MNB/DYRK protein kinase		

NM_031373 NP_056549. 1	U:2.35 F:2.9	Mm.250418	NP_031372.2	opioic growth factor receptor; 7-60 protein; zeta-type opioic receptor	569	e-162
			Q9NZT2	Opioic growth factor receptor (OGFr) (Zeta-type opioic receptor)	569	e-162
			AAH14137.1	OGFR protein	566	e-161
			AAF64404.1	opioic growth factor receptor	560	e-159
			AAF64405.1	opioic growth factor receptor	558	e-158
			AAF64406.1	opioic growth factor receptor	547	e-155
			CAC12749.1	dJ885L7.3.1 (opioic growth factor receptor (7-60 protein), isoform 1)	539	e-153
			CAC28882.1	dJ885L7.3.2 (opioic growth factor receptor (7-60 protein), isoform 2)	520	e-147
			BAB15775.1	FLJ00084 protein	519	e-147
			AAD03737.1	7-60	498	e-140
			AAD03745.1	7-60	498	e-140
NM_021566 NP_067541. 1	U:2.34 F:5.13	Mm.34459	NP_065166.2	junctophilin 2 isoform 1	823	0
			Q9BR39	Junctophilin 2 (Junctophilin type 2) (JP-2)	823	0
			CAC36289.1	dJ1108D11.1 (novel protein similar to C. elegans T22C1.7)	532	e-150
			AAH43206.2	JPH2 protein	483	e-136

NM_011229	P35239	Mm.12815	U:2.33 F:3.25	NP_065698.	1	junctophilin 1; mitsugumin72; junctophilin type1	454	e-127
				Q9HDC5	1	Junctophilin 1 (Junctophilin type 1) (JP-1)	454	e-127
				BAB11983.1	1	Junctophilin type3	428	e-119
				CAD97825.1	1	hypothetical protein	427	e-119
				AAH36533.1	1	Junctophilin 3	426	e-118
				NP_065706.	1			
				2	1	junctophilin 3; junctophilin type 3; trinucleotide repeat containing 22	425	e-118
				Q8WXH2	1	Junctophilin 3 (Junctophilin type 3) (JP-3)	425	e-118
				BAB47460.1	1	KIAA1831 protein	307	7e-083
				NP_115828.	1			
				1	1	junctophilin like 1	307	7e-083
				AAH55429.1	1	Junctophilin like 1	307	7e-083
				AAH56422.1	1	AAH56422.1	400	e-111
				NP_002859.	1			
				1	1	RAB5B, member RAS oncogene family	400	e-111
				P35239	1	Ras-related protein Rab-5B	400	e-111
				A43925	1	GTP-binding protein Rab5b - human	400	e-111
				CAA38653.1	1	ras related protein Rab5b	400	e-111
				AAM21085.1	1	small GTP binding protein RAB5B	400	e-111
				CAD97650.1	1	hypothetical protein	400	e-111
				AAH40143.1	1	Similar to RAB5B, member RAS oncogene family	400	e-111
				AAH65298.1	1	Unknown (protein for IMAGE:6146668)	400	e-111
				AAH50558.1	1	RAB5B, member RAS oncogene family	400	e-111
				P51148	1	RB5C_HUMAN Ras-related protein Rab-5C (RAB5L) (L1880)	348	4e-096
				AAF66594.1	1	small GTPase	348	4e-096
				AAM21086.1	1	small GTP binding protein RAB5C	348	4e-096

NP 058068

	NP_003976.	tyrosine kinase, non-receptor, 1; tyrosine kinase non-receptor 1;	1	tyrosine kinase non-receptor 1	332	3e-090
	AAC50427.1	tyrosine kinase			332	3e-090
	NP_002022.	fyn-related kinase; tyrosine-protein kinase FRK; nuclear tyrosine				
	1	protein kinase RAK; PTK5 protein tyrosine kinase 5:			210	1e-053
	P42685	Tyrosine-protein kinase FRK (Nuclear tyrosine protein kinase RAK)			210	1e-053
	I38396	protein-tyrosine kinase (EC 2.7.1.112) FRK - human			210	1e-053
	AAA18284.1	SRC-like tyrosine kinase			210	1e-053
	AAH12916.1	Fyn-related kinase			210	1e-053
	2006289A	src-like Tyr kinase			210	1e-053
	AAC50116.1	Rak			210	1e-053
	CAC27542.1	bA702N8.1 (fym-related kinase)			210	1e-053
NM_011334			U:-2.32			
I48294	Mm.297883	F:-2.56			1363	0
	P51793	Chloride channel protein 4 (ClC-4)			1363	0
	BAA77327.1	chloride channel protein 4			1363	0
	AAD50981.1	chloride channel CLC4			1363	0
	NP_001821.					
	1	chloride channel 4			1355	0
	I37242	chloride channel - human			1355	0
	CAA54417.1	chloride channel			1355	0
	AAB95161.1	chloride channel protein 3			1119	0
	AAD51034.1	chloride channel 3			1119	0
	P51790	Chloride channel protein 3 (ClC-3)			1114	0
	CAA55281.1	chloride channel 3			1114	0
	NP_001820.					
	1	chloride channel 3; ClC-3			1114	0
	I37240	chloride channel protein 3, long form - human			1114	0
	CAA55280.1	chloride channel 3			1114	0

[illegible]

IMD2_HUMAN Inosine-5'-monophosphate dehydrogenase 2 (IMP dehydrogenase 2)				
P12268	(IMPDH-II) (IMPD 2)			868
A31997	IMP dehydrogenase (EC 1.1.1.205) II - human			868
Chain A, Ternary Complex Of Human Type-II Inosine Monophosphate Dehydrogenase With 6-Cl-Imp And Selenazole Adenine				
Dinucleotide				
pdb 1B3O A				868
Chain B, Ternary Complex Of Human Type-II Inosine Monophosphate Dehydrogenase With 6-Cl-Imp And Selenazole Adenine				
Dinucleotide				
pdb 1B3O B				868
AAA67054.1	inosine monophosphate dehydrogenase type II			868
AAB70699.1	inosine monophosphate dehydrogenase type II			868
AAH06124.1	IMP (inosine monophosphate) dehydrogenase 2			868
AAH12840.1	IMP (inosine monophosphate) dehydrogenase 2			868
AAH15567.1	IMP (inosine monophosphate) dehydrogenase 2			868
XP_069825.4	similar to Impdh1 protein			865
P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)				
(Purinergic receptor)				
P41231				578
AAH28135.1	Purinergic receptor P2Y2			578
AAN01279.1	purinergic receptor P2RY2			578
NP_002555.2	purinergic receptor P2Y2; purinoceptor P2Y2; P2U nucleotide receptor; P2Y purinoceptor 2; P2U purinoceptor 1; ATP receptor			578
NP_788085.1	purinergic receptor P2Y2; purinoceptor P2Y2; P2U nucleotide receptor; P2Y purinoceptor 2; P2U purinoceptor 1; ATP receptor			578
NP_788086.1	purinergic receptor P2Y2; purinoceptor P2Y2; P2U nucleotide receptor; P2Y purinoceptor 2; P2U purinoceptor 1; ATP receptor			578
AAC04923.1	P2U nucleotide receptor			576

NM_007483	AAH12104.1	Purinergic receptor P2Y2	576	e-164
	A54946	P-2U nucleotide receptor - human	563	e-160
	AAC50347.1	uridine nucleotide receptor	303	8e-082
	NP_002556.1	pyrimidinergic receptor P2Y4; P2Y purinoceptor 4; uridine nucleotide receptor	302	2e-081
	P51582	P2Y purinoceptor 4 (P2Y4) (Uridine nucleotide receptor) (UNR) (P2P)	302	2e-081
	S68679	G protein-coupled receptor - human	302	2e-081
NP_031509.1	CAA62963.1	uridine nucleotide receptor	302	2e-081
	CAA65415.1	G protein coupled receptor	302	2e-081
	ras homolog gene family, member B; Aplysia RAS-related homolog 6 (oncogene RHO H6); Aplysia ras-related homolog 6; RhoB; RAS homolog gene family, member B (oncogene RHO H6)			
	NP_004031.1	member B (oncogene RHO H6)	402	e-112
	P01121	RHOB_HUMAN Transforming protein RhoB (H6)	402	e-112
	TVHURH	GTP-binding protein rhoB	402	e-112
NP_001655.1	CAA29968.1	rhoB	402	e-112
	AAM21118.1	AF498971_1 small GTP binding protein RhoB	402	e-112
	AAA36565.1	rho protein	347	5.00e-96
	NP_001655.1	ras homolog gene family, member A; Aplysia ras-related homolog 12; Rho12; RhoA; Ras homolog gene family, member A (oncogene RHO H12)	337	5.00e-93
	P06749	RHOA_HUMAN Transforming protein RhoA (H12)	337	5.00e-93
	TVHU12	GTP-binding protein rhoA	337	5.00e-93
XP_209223.1	CAA28690.1	ORF (AA 1-193)	337	5.00e-93
	AAC33178.1	GTP-binding protein	337	5.00e-93
	AAH01360.1	ras homolog gene family, member A	337	5.00e-93
	AAH05976.1	ras homolog gene family, member A	337	5.00e-93
	AAM21117.1	AF498970_1 small GTP binding protein RhoA	337	5.00e-93
	XP_209223.1	similar to Transforming protein RhoC (H9)	336	1.00e-92

ras homolog gene family, member C; Aplysia RAS-related homolog 9 (oncogene			
NP_786886.	RHO H9); Aplysia ras-related homolog 9; RhoC; RAS homolog gene family,		
1	member C (oncogene RHO H9)	336	1.00e-92
P08134	RHOC_HUMAN Transforming protein RhoC (H9)	336	1.00e-92
TVHURC	GTP-binding protein rhoC	336	1.00e-92
CAA29969.1	rhoC coding region (AA 1-193)	336	1.00e-92
AAC33179.1	GTPase	336	1.00e-92
AAH07245.1	ras homolog gene family, member C	336	1.00e-92
AAH09177.1	ras homolog gene family, member C	336	1.00e-92
AAM21119.1	AF498972_1 small GTP binding protein Rho	336	1.00e-92
B Chain B, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs			
1LB1	In Complex With Rhoa	335	2.00e-92
D Chain D, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs			
1LB1	In Complex With Rhoa	335	2.00e-92
F Chain F, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs			
1LB1	In Complex With Rhoa	335	2.00e-92
H Chain H, Crystal Structure Of The Dbl And Pleckstrin Homology Domains Of Dbs			
1LB1	In Complex With Rhoa	335	2.00e-92
1FTN	Crystal Structure Of The Human RhoGDP COMPLEX	334	6.00e-92
1CC0	A Chain A, Crystal Structure Of The Rhoa.Gdp-Rhogdi Complex	333	9.00e-92
1CC0	C Chain C, Crystal Structure Of The Rhoa.Gdp-Rhogdi Complex	333	9.00e-92
AAA50612.1	multidrug resistance protein	331	5.00e-91
1A2B	Human Rhoa Complexed With Gtp Analogue	328	3.00e-90
A Chain A, Crystal Structure Of Human Rhoa Complexed With The Effector			
1CXZ	Domain Of The Protein Kinase PknPRK1	328	3.00e-90
1DPF	A Chain A, Crystal Structure Of A Mg-Free Form Of Rhoa Complexed With Gdp	320	8.00e-88
AF316872			
NP_115794.			
1		801	0
U:+2.26	NP_115785.		
Mm.18539	F:3.65		
	1		
	PTEN induced putative kinase 1; protein kinase BRPK		

NM_011134	AAK28062.1	protein kinase BRPK	801	0
	BAB55647.1	PTEN induced putative kinase 1	801	0
	AAH28215.1	PTEN induced putative kinase 1	798	0
	AAH09534.1	PINK1 protein	484	e-136
	BAC11484.1	unnamed protein product	408	e-113
NP_035264.	AAB25717.1	paraoxonase/arylesterase	594	e-169
	NP_000437.			
	3	paraoxonase 1; Paraoxonase	593	e-169
	CAA94728.1	serum arylalkylphosphatase	593	e-169
	AAA97957.1	serum arylalkylphosphatase	593	e-169
1	BAA12327.1	serum arylalkylphosphatase	593	e-169
	AAC35293.1	serum paraoxonase/arylesterase 1	593	e-169
	AAM97935.1	paraoxonase 1	593	e-169
		Serum paraoxonase/arylesterase 1 (PON 1) (Serum arylalkylphosphatase 1)		
	P27169	(A-esterase 1) (Aromatic esterase 1) (K-45)	593	e-169
	A45451	arylalkylphosphatase (EC 3.1.8.1) precursor - human	593	e-169
	AAB59538.1	serum paraoxonase	593	e-169
	AAB41835.1	paraoxonase	593	e-169
	AAB27714.2	paraoxonase; PON	593	e-169
	AAB27899.1	paraoxonase B-type/arylesterase B-type precursor	593	e-169
	AAA60142.1	serum paraoxonase	589	e-168
	1921159B	paraoxonase	588	e-168
	AAA60143.1	serum paraoxonase	570	e-162
	AAC62431.1	unknown	474	e-133
	AAO18083.1	paraoxonase 2	474	e-133

		Serum paraoxonase/arylesterase 2 (PON 2) (Serum Serum		
	Q15165	paraoxonase/arylesterase 2 (PON 2) (Serum esterase 2)	472	e-133
	NP_000296.			
	1	paraoxonase 2	471	e-132
	AAC27944.1	paraoxonase	471	e-132
AK010568	U:+2.23			
I49605	Mm.275206	unnamed protein product	702	0
	NP_079523.			
	2	hypothetical protein MGC5601	696	0
	BAC03869.1	unnamed protein product	696	0
	NP_115545.			
	3	putative acyl-CoA dehydrogenase	496	e-140
	CAE55233.1	putative acyl-CoA dehydrogenase	495	e-139
	AAH19607.1	FLJ12592 protein	406	e-113
	BAB14158.1	unnamed protein product	405	e-112
	NP_002197.			
NIM_008398	U:+2.19	integrin alpha 7 precursor	1882	0
I61186	Mm.179747	integrin alpha-7 chain precursor - human	1882	0
	JC5950	integrin alpha-7	1882	0
	AAC39708.1	integrin alpha-7	1882	0
	AAC80458.1	integrin alpha-7	1882	0
	CAB41535.1	integrin alpha-7	1882	0
	AAC18968.1	integrin alpha 7	1878	0
	AAH50280.1	Integrin alpha 7 precursor	1878	0
	Q13683	Integrin alpha-7 precursor	1861	0
	CAB41534.1	Integrin alpha 7 chain	1804	0
	AAQ89241.1	ITGA7	1804	0
	P23229	Integrin alpha-6 precursor (VLA-6) (CD49f)	937	0
	A41543	Integrin alpha-6 chain precursor, splice form B - human	921	0
	AAD48469.1	Integrin alpha 6	905	0

Accession	Gene	Protein	Length
NP_000201.1	1	integrin alpha chain, alpha 6	905
CAA37655.1	1	integrin alpha 6 (or alpha E) protein	905
CAA42099.1	1	integrin alpha6 subunit	904
U62559	U:2.18	solute carrier family 20, member 2; gibbon ape leukemia virus receptor 2; murine leukemia virus, amphotropic, receptor for	e-108
AAB06046.1	F:3.12	leukemia virus receptor 2 - human	390
A37000	1	leukemia virus receptor 2	390
AAA18018.1	1	Solute carrier family 20 (phosphate transporter), member 2	390
AAH28600.1	1	gibbon ape leukemia virus receptor 1	317
AAD20286.1	1	solute carrier family 20 (phosphate transporter), member 1; Glvr-1;	9e-087
NP_005406.1	1	PIT-1; gibbon ape leukemia virus receptor 1	317
AAH19944.1	1	Solute carrier family 20 (phosphate transporter), member 1	317
I52822	1	leukemia virus receptor 1 - human	317
AAA52572.1	1	leukemia virus receptor 1	317
NM_010719	1	Hormone sensitive lipase (HSL)	1187
NP_034849.1	1	hormone-sensitive lipase	1187
Mm.298162	F:4.34	hormone-sensitive lipase testicular isoform	1187
NP_005348.1	1	hormone-sensitive lipase; hormone-sensitive lipase testicular isoform	1187
A47546	1	triacylglycerol lipase (EC 3.1.1.3), hormone-sensitive - human	1140
NM_010091	1	dishevelled 1 isoform a	912
NP_034221.1	1	Segment polarity protein dishevelled homolog DVL-1 (Dishevelled-1)	910
Mm.298109	F:3.45	(DSH homolog 1)	

AAB65242.1	dishevelled 1	910	0
	Segment polarity protein dishevelled homolog DVL-1-like		
P54792	(Dishevelled-1-like) (DSH homolog 1-like)	900	0
AAC50682.1	cytoplasmic phosphoprotein	900	0
AAH17225.1	DVL1 protein	666	0
	Segment polarity protein dishevelled homolog DVL-3 (Dishevelled-3)		
Q92997	(DSH homolog 3)	603	e-172
AAB65244.1	dishevelled 3	603	e-172
BAA13199.2	KIAA0208	603	e-172
NP_004414.			
2	dishevelled 3; dishevelled 3 (homologous to Drosophila dsh)	600	e-171
JC5763	dishevelled protein 3 - human	600	e-171
AAB84228.1	dishevelled 3	600	e-171
AAH32459.1	Dishevelled 3	598	e-170
AAB47447.1	cytoplasmic phosphoprotein	583	e-166
NP_057231.			
1	protein phosphatase methyltransferase-1	417	e-116
AAD44976.1	protein phosphatase methyltransferase-1	417	e-116
AAH03046.1	protein phosphatase methyltransferase-1	417	e-116
AAH50705.1	protein phosphatase methyltransferase-1	417	e-116
BAA91661.1	unnamed protein product	417	e-116
NM_011351			
NP_082568	Mm.177502	1361	0
	F:2.95	1353	0
	U:2.15		
	U:2.14		
	F:4.87		
	Mm.23662		
	KIAA1869 protein		
	Semaphorin 6C precursor (Semaphorin Y) (Sema Y)		

AAL72098.1	semaphorin Y short isoform 1	1353	0
NP_112175.2	semaphorin Y; sema domain, transmembrane domain (TM), and cytoplasmic domain, 6C	1350	0
BAB20670.1	semaphorin Y	1349	0
AAL72100.1	semaphorin Y	1337	0
AAL72099.1	semaphorin Y short isoform 2	1238	0
NP_705872.1	semaphorin 6D isoform 5 precursor	570	e-162
NP_705869.1	semaphorin 6D isoform 2 precursor	568	e-161
AAM69450.1	semaphorin 6D isoform 2	568	e-161
NP_705870.1	semaphorin 6D isoform 3 precursor	568	e-161
AAM69451.1	semaphorin 6D isoform 3	568	e-161
NP_705871.1	semaphorin 6D isoform 4 precursor	568	e-161
AAM69452.1	semaphorin 6D isoform 4	568	e-161
NM_032418	U:+2.14		
NP_115794	Mm.6529		
AAH62553.1	DMPK protein	927	0.0
AAC14449.1	myotonic dystrophy kinase	926	0.0
B49364	protein kinase (EC 2.7.1.37), myotonic dystrophy-associated	910	0.0
AAC14448.1	myotonic dystrophy kinase	910	0.0
AAA36206.1	protein kinase	910	0.0
NP_004400.3	myotonic dystrophy protein kinase; dystrophin myotonia 1	908	0.0
	myotonic dystrophy kinase, DM-kinase {C-terminal, alternatively spliced, clone delta II} [human, Peptide Partial, 616 aa]	903	0.0
AAB26549.1	DMK_HUMAN Myotonin-protein kinase (Myotonic dystrophy protein kinase)		
Q09013	(MDPK)(DM-kinase) (DMK) (DMPK) (MT-PK)	884	0.0

NM_007383 l49605	U:-2.14 F:2.51 Mm.18759	AAA75236.1	myotonin-protein kinase, Form I	884	0.0
		AAA75239.1	myotonin-protein kinase, Form VI	867	0.0
		AAA64884.1	protein kinase	827	0.0
		AAA75240.1	myotonin-protein kinase, Form II,III,IV	822	0.0
		AAB31800.1	myotonin protein kinase; MTPK	820	0.0
		NP_000008.			
		1	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain precursor	680	0
			Acyl-CoA dehydrogenase, short-chain specific, mitochondrial precursor		
		P16219	(SCAD) (Butyryl-CoA dehydrogenase)	680	0
			acyl-CoA dehydrogenase (EC 1.3.99.3) precursor, short-chain-specific		
		A30605	- human	680	0
		AAA60307.1	short chain acyl-CoA dehydrogenase precursor (EC 1.3.99.2)	680	0
		CAB02492.1	acyl-CoA dehydrogenase	680	0
		AAD00552.1	short chain acyl CoA dehydrogenase	680	0
		1704375A	short chain acyl-CoA dehydrogenase	680	0
		AAH25963.1	Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain precursor	678	0
		CAD38535.2	hypothetical protein	273	7e-073
		NP_001600.	acyl-Coenzyme A dehydrogenase, short/branched chain precursor,		
		1	2-methyl branched chain acyl-CoA dehydrogenase;	273	7e-073
			2-methylbutyryl-CoA dehydrogenase		
			Acyl-CoA dehydrogenase, short/branched chain specific, mitochondrial		
			precursor (SBCAD) (2-methyl branched chain acyl-CoA		
			dehydrogenase) (2-MEBCAD) (2-methylbutyryl-coenzyme A		
		P45954	dehydrogenase) (2-methylbutyryl-CoA dehydrogenase)	273	7e-073
			acyl-CoA dehydrogenase (EC 1.3.99.-) short/branched chain specific		
		A55680	precursor - human	273	7e-073
		AAA74424.1	acyl-CoA dehydrogenase	273	7e-073
		AAF97921.1	short/branched chain acyl-CoA dehydrogenase	273	7e-073
		AAH13756.1	Acyl-Coenzyme A dehydrogenase, short/branched chain precursor	273	7e-073

AAF63626.1	medium-chain acyl-CoA dehydrogenase	258	2e-068
NP_000007.1	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain; medium-chain acyl-CoA dehydrogenase	258	2e-068
P11310	ACDM_HUMAN Acyl-CoA dehydrogenase, medium-chain specific, mitochondrial precursor (MCAD)	258	2e-068
DEHUCM	acyl-CoA dehydrogenase (EC 1.3.99.3) precursor, medium-chain-specific, mitochondrial [validated] - human	258	2e-068
AAA51566.1	medium-chain acyl-CoA dehydrogenase (EC 1.3.99.3)	258	2e-068
AAA59567.1	medium-chain acyl-CoA dehydrogenase	258	2e-068
AAH05377.1	Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	258	2e-068
1EGE A	Chain A, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase	257	5e-068
1EGE B	Chain B, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase	257	5e-068
1EGE C	Chain C, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase	257	5e-068
1EGE D	Chain D, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase	257	5e-068
1EGD A	Chain A, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase	254	3e-067
1EGD B	Chain B, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase	254	3e-067
1EGD C	Chain C, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase	254	3e-067
1EGD D	Chain D, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase	254	3e-067
1EGC A	Chain A, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase Complexed With Octanoyl-CoA	254	3e-067

1EGC B	Chain B, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase Complexed With Octanoyl-CoA	254	3e-067
1EGC C	Chain C, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase Complexed With Octanoyl-CoA	254	3e-067
1EGC D	Chain D, Structure Of T255e, E376g Mutant Of Human Medium Chain Acyl-CoA Dehydrogenase Complexed With Octanoyl-CoA	254	3e-067
1IVH A	Chain A, Structure Of Human Isovaleryl-CoA Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity	248	2e-065
1IVH B	Chain B, Structure Of Human Isovaleryl-CoA Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity	248	2e-065
1IVH C	Chain C, Structure Of Human Isovaleryl-CoA Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity	248	2e-065
1IVH D	Chain D, Structure Of Human Isovaleryl-CoA Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity	248	2e-065
AA596988	U:2.13		
Q9ER41	Mm.249164	F:3.11	
	1	torsin family 1, member B (torsin B)	184
	O14657	Torsin B precursor (Torsin family 1 member B)	184
	AAG50271.1	FKSG18	184
	CAC88165.1	bA409K20.1.1 (torsin family 1, member B (torsin B) (DQ1))	184
	AAH15578.1	Torsin family 1, member B (torsin B)	184
AK010815	U:2.11		
BAB27199.1	N/A	F:3.47	
	AAD03162.1	R30923_1	425
	NP_219483.		
1	hypothetical gene MGC19595		407

NM_011571	JC6534	Mm.10154	F:2.85	U:+2.10
	AH38448.1 NP_006276.	TESK1 protein		
	1	testis-specific protein kinase 1		
	Q15569	TES1 Testis-specific protein kinase 1 (Testicular protein kinase 1)		
	BAA09459.1	TESK1		
	AAM50515.1	testis-specific kinase-1		
	Q96S53	TES2 Testis-specific protein kinase 2 (Testicular protein kinase 2)		
	BAB62909.1	testicular protein kinase 2		
	NP_009101.			
	1	testis-specific protein kinase 2		
	CAB41970.1	protein kinase		
	AH33085.1	TESK2 protein		
	AAM77909.1	testis specific kinase-1		
	AAM50517.1	testis-specific kinase-1		
	AAM50516.1	testis-specific kinase-1		
	AAL49755.1	testis-specific kinase 1		
NM_019707				
	NP_001248.	cadherin 13 preproprotein; H-cadherin; heart-cadherin; T-cadherin;		
	1	truncated-cadherin; T-cad; P105		
		CADD_HUMAN Cadherin-13 precursor (Truncated-cadherin) (T-cadherin) (T-cad)		
	P55290	(Heart-cadherin) (H-cadherin) (P105)		
	B38992	cadherin 13 precursor		
	AAA35624.1	cadherin-13		
	AAB18911.1	H-cadherin		
	AAB18912.1	H-cadherin		
	BAA32411.1	H-cadherin		
	AHH28624.1	cadherin 13, H-cadherin (heart)		
NP_062681.				
1	Mm.24700			

	AAH30653.1	Unknown (protein for MGC:33162)	1293	0
	IJHUCN	cadherin 2 precursor	510	e-144
	CAA38213.1	precursor protein	510	e-144
	P19022	CAD2_HUMAN Neural-cadherin precursor (N-cadherin) (Cadherin-2)	508	e-143
	NP_001783.	cadherin 2, type 1 preproprotein; N-cadherin 1; cadherin 2, N-cadherin (neuronal);		
	2	neural cadherin; calcium-dependent adhesion protein, neuronal	508	e-143
	AAB22854.1	N-cadherin	508	e-143
	AAH36470.1	cadherin 2, type 1, N-cadherin (neuronal)	503	e-142
	NP_001785.	cadherin 4, type 1 preproprotein; cadherin 4, R-cadherin (retinal); R-cadherin;		
	2	retinal cadherin	479	e-135
	P55283	CAD4_HUMAN Cadherin-4 precursor (Retinal-cadherin) (R-CAD)	474	e-133
	C38992	cadherin 4 precursor	474	e-133
	AAA35627.1	cadherin-4	474	e-133
	AAA03236.1	N-cadherin	472	e-132
NM_009964				
	NP_034094.			
1			337	1.00e-92
	1	crystallin, alpha B; heat-shock 20 kD like-protein		
	1	CRAB_HUMAN Alpha crystallin B chain (Alpha(B)-crystallin) (Rosenthal fiber	336	3.00e-92
	1	component)	336	3.00e-92
	1	alpha-crystallin chain B	336	3.00e-92
	1	alpha-B2-crystallin	336	3.00e-92
	1	alpha B-crystallin	336	3.00e-92
	1	crystallin, alpha B	336	3.00e-92
NM_011750				
	NP_035880.			
1			702	0
	1	SF1-Bo isoform		

Accession	Protein Name	Length
Q15637	Splicing factor 1 (Zinc finger protein 162) (Transcription factor ZFM1) (Zinc finger gene in MEN1 locus) (Mammalian branch point binding protein mBBP) (BBP)	702
CAA70018.1	SF1-H1 isoform	702
AAH08080.1	SF1 protein	702
AAH08724.1	SF1 protein	702
AAH20217.1	SF1 protein	702
AAB03514.1	transcription factor ZFM1	702
G02919	transcription factor ZFM1 - human	702
AAB04033.1	transcription factor ZFM1	702
NP_004621.		
1	splicing factor 1; zinc finger protein 162	697
BAA05117.1	ZFM1 protein	697
BAA05116.1	ZFM1 protein alternatively spliced product	697
AAH38446.1	SF1 protein	683
CAA03883.1	splicing factor SF1	596
1K1G	Chain A, Structural Basis For Recognition Of The Intron Branch Site Rna By Splicing Factor 1	254
NM_019572		3e-067
NP_062518.		
1		
Mm.259829	HDAC7A protein	1397
F-3.22	histone deacetylase	1379
	histone deacetylase 7A variant 3	1370
NP_057680.		
2	histone deacetylase 7A isoform b	1360
NP_056216.		
1	histone deacetylase 7A isoform a	1352
Q8WUJ4	Histone deacetylase 7a (HD7a)	1352
T17245	hypothetical protein DKFZp586J0917.1 - human (fragment)	1264

U89415		CAB55935.1	hypothetical protein	1264	0
P58252	Mm.289431	AAF63491.1	histone deacetylase 7	1217	0
		AAH20505.2	HDAC7A protein	1101	0
		AAP88773.1	histone deacetylase 7A	964	0
		BAA91545.1	unnamed protein product	959	0
	U:-+2.02				
	F:2.92	AAH06547.1	EEF2 protein	444	e-125
		NP_001952.1	eukaryotic translation elongation factor 2; polypeptidyl-tRNA translocase	444	e-125
		P13639	Elongation factor 2 (EF-2)	444	e-125
		EFHU2	translation elongation factor eEF-2 - human	444	e-125
		CAA35829.1	elongation factor 2	444	e-125
		CAA77750.1	human elongation factor 2	444	e-125
NM_011306	U:-+2.02				
NP_035436	Mm.1243	AAA60293.1	retinoid X receptor beta	634	0
	F:2.88	NP_068811.1			
		1	retinoid X receptor, beta; MHC class I promoter binding protein	634	0
		P28702	Retinoic acid receptor RXR-beta	634	0
		CAA45087.1	retinoic acid X receptor b	634	0
		AAC18599.1	retinoic X receptor B	634	0
		CAA20239.1	dJ1033B10.11 (retinoid X receptor beta)	634	0
		AAD13794.1	retinoic X receptor beta	634	0
		AAH01167.1	retinoic X receptor beta	634	0
		AAP35944.1	retinoic X receptor beta	634	0
		S37781	retinoid X receptor beta - human	634	0
		AAH63827.1	RXRA protein	526	e-149
		NP_002948.1			
		1	retinoid X receptor, alpha	526	e-149
		P19793	RXRA_HUMAN Retinoic acid receptor RXR-alpha	526	e-149

S09592	retinoid X receptor alpha [validated] - human	526	e-149
CAA36982.1	unlabeled protein product	526	e-149
1609194A	retinoic acid receptor RXRalpha	526	e-149
NP_008848.			
1	retinoid X receptor, gamma	494	e-139
P48443	Retinoic acid receptor RXR-gamma	494	e-139
AAA80681.1	retinoid X receptor-gamma	494	e-139
CAC00596.1	bA280O1.2 (retinoid X receptor, gamma (NR2B3))	494	e-139
AAH12063.1	Retinoid X receptor, gamma	494	e-139
1LBD	Ligand-Binding Domain Of The Human Nuclear Receptor Rxr-Alpha Chain A, The Structure Of The Human Retinoid-X-Receptor Beta Ligand Binding Domain In Complex With The Specific Synthetic Agonist Lg100268	419	e-117
1H9UJA	Chain B, The Structure Of The Human Retinoid-X-Receptor Beta Ligand Binding Domain In Complex With The Specific Synthetic Agonist Lg100268	416	e-115
1H9UJB	Chain C, The Structure Of The Human Retinoid-X-Receptor Beta Ligand Binding Domain In Complex With The Specific Synthetic Agonist Lg100268	416	e-115
1H9UJC	Chain D, The Structure Of The Human Retinoid-X-Receptor Beta Ligand Binding Domain In Complex With The Specific Synthetic Agonist Lg100268	416	e-115
1H9UJD	Agonist Lg100268	416	e-115
I38104	MHC class I promoter binding protein - human (fragment)	415	e-115
CAA46456.1	MHC class I promoter binding protein	415	e-115
	Chain A, The 2.1 Angstrom Resolution Crystal Structure Of The Heterodimer Of The Human Rxralpha And Ppargamma Ligand Binding Domains Respectively Bound With 9-Cis Retinoic Acid And Rosiglitazone And Co-Activator Peptides.	408	e-113

1FM6 U	Chain U, The 2.1 Angstrom Resolution Crystal Structure Of The Heterodimer Of The Human Rxralpha And Ppargamma Ligand Binding Domains Respectively Bound With 9-Cis Retinoic Acid And Rosiglitazone And Co-Activator Peptides. Chain A, The 2.1 Angstrom Resolution Crystal Structure Of The Heterodimer Of The Human Rxralpha And Ppargamma Ligand Binding Domains Respectively Bound With 9-Cis Retinoic Acid And Gl262570 And Co-Activator Peptides.	408	e-113
1FM9 A	Chain A, The 2.0 Angstrom Resolution Crystal Structure Of The Rxralpha Ligand Binding Domain Tetramer In The Presence Of A Non-Activating Retinoic Acid Isomer.	408	e-113
1G5Y A	Chain B, The 2.0 Angstrom Resolution Crystal Structure Of The Rxralpha Ligand Binding Domain Tetramer In The Presence Of A Non-Activating Retinoic Acid Isomer.	408	e-113
1G5Y B	Chain C, The 2.0 Angstrom Resolution Crystal Structure Of The Rxralpha Ligand Binding Domain Tetramer In The Presence Of A Non-Activating Retinoic Acid Isomer.	408	e-113
1G5Y C	Chain D, The 2.0 Angstrom Resolution Crystal Structure Of The Rxralpha Ligand Binding Domain Tetramer In The Presence Of A Non-Activating Retinoic Acid Isomer.	408	e-113
1G5Y D	Chain A, The 2.5 Angstrom Resolution Crystal Structure Of The Rxralpha Ligand Binding Domain In Tetramer In The Absence Of Ligand	408	e-113
G1U A	Chain B, The 2.5 Angstrom Resolution Crystal Structure Of The Rxralpha Ligand Binding Domain In Tetramer In The Absence Of Ligand	408	e-113
G1U B		408	e-113

			Chain C, The 2.5 Angstrom Resolution Crystal Structure Of The Ralpha Ligand Binding Domain In Tetramer In The Absence Of Ligand	408	e-113
			Chain D, The 2.5 Angstrom Resolution Crystal Structure Of The Ralpha Ligand Binding Domain In Tetramer In The Absence Of Ligand	408	e-113
			Chain A, The 2.3 Angstrom Resolution Crystal Structure Of The Heterodimer Of The Human Ppargamma And Ralpha Ligand Binding Domains Respectively Bound With Gw409544 And 9-Cis Retinoic Acid And Co-Activator Peptides.	408	e-113
			v-ets erythroblastosis virus E26 oncogene homolog 2; Oncogene ETS-2; v-ets avian erythroblastosis virus E2 oncogene homolog 2; v-ets avian erythroblastosis virus E26 oncogene homolog 2		
NM_011809	U:+2.02	NP_005230.		868	0
P15037	Mm.290207	1	2; human erythroblastosis virus oncogene homolog 2	868	0
		P15036	C-ets-2 protein	868	0
		TVHUE2	transcription factor ets-2 - human	868	0
		AAA52412.1	ets2 protein	868	0
		AAB94057.1	erythroblastosis virus oncogene homolog 2 protein	868	0
		AAH17040.1	V-ets erythroblastosis virus E26 oncogene homolog 2	868	0
		AAH42954.1	V-ets erythroblastosis virus E26 oncogene homolog 2	868	0
		AAP35484.1	V-ets erythroblastosis virus E26 oncogene homolog 2	868	0
		CAB90468.1	human erythroblastosis retrovirus oncogene homologue 2	536	e-151
		CAE45783.1	hypothetical protein	433	e-121

[illegible]

NM_008599	U:2.01	NP_000656.				
JH0314	Mm.255464	F:3.16	1	acetylcholinesterase hydrophilic form precursor	1065	0
			P22303	Acetylcholinesterase precursor (AChE)	1065	0
				acetylcholinesterase (EC 3.1.1.7) precursor, brain splice form - human		
			A39256		1065	0
			AAA68151.1	acetylcholinesterase	1065	0
			AAP22365.1	unknown	1065	0
				Chain A, Crystal Structure Of Mutant E202q Of Human Acetylcholinesterase Complexed With Green Mamba Venom		
			1F8U	Peptide Fasciculin-II	1057	0
			NP_056646.			
			1	acetylcholinesterase PI-linked form precursor	978	0
			AAP22364.1	unknown	978	0
				Chain A, Human Acetylcholinesterase Complexed With Fasciculin-II, Glycosylated Protein		
			1B41		963	0
			NP_000046.			
			1	butyrylcholinesterase precursor	627	e-179
				Cholinesterase precursor (Acylcholine acylhydrolase) (Choline esterase II) (Butyrylcholine esterase)		
			P06276	(Pseudocholinesterase)	627	e-179
			ACHU	cholinesterase (EC 3.1.1.8) precursor [validated] - human	627	e-179
			AAA98113.1	cholinesterase (EC 3.1.1.8)	627	e-179
			AAA52015.1	butyrylcholinesterase (EC 3.1.1.8)	627	e-179
			AAA99296.1	butyrylcholinesterase	627	e-179
			AAH18141.1	Butyrylcholinesterase precursor	627	e-179
			AAO32948.1	apoptosis-related acetylcholinesterase	600	e-171
			1P0I	Chain A, Crystal Structure Of Human Butyryl Cholinesterase	568	e-161
				Chain A, Crystal Structure Of Human Butyryl Cholinesterase In Complex With A Choline Molecule		
			1P0M		568	e-161

Chain A, Crystal Structure Of Soman-Aged Human Butyryl Cholinesterase					
1P0P	In Complex With The Substrate Analog Butyrylthiocholine			568	e-161
1P0Q	Chain A, Crystal Structure Of Soman-Aged Human Butyryl Cholinesterase			568	e-161
AAF71232.1	neurologilin 3 isoform			315	2e-085
AAH51715.1	Neurologilin 3			315	2e-085
NP_061850.					
1	neurologilin 3			313	1e-084
AAF71230.1	neurologilin 3 isoform HNL3			313	1e-084
NM_010518					
NP_034648.		U:-2.01			
1		F:3.15	Mm.578	522	e-147
	insulin-like growth factor binding protein 5				
	Insulin-like growth factor binding protein 5 precursor (IGFBP-5)				
P24593	(IBP-5) (IGF-binding protein 5)			522	e-147
A53748	insulin-like growth factor-binding protein 5 precursor - human			522	e-147
AAA53505.1	Insulin-like growth factor binding protein 5			522	e-147
AAD04730.1	insulin-like growth factor binding protein 5			522	e-147
	[Human insulin-like growth factor binding protein 5 (IGFBP5) gene],				
AAA27051.1	gene product			522	e-147
AAC09368.1	Insulin-like growth factor binding protein 5			522	e-147
AAH11453.1	Insulin-like growth factor binding protein 5			522	e-147
AAH64987.1	Insulin-like growth factor binding protein 3			233	2e-060
NP_000589.					
1	insulin-like growth factor binding protein 3			233	2e-060
	Insulin-like growth factor binding protein 3 precursor (IGFBP-3)				
P17936	(IBP-3) (IGF-binding protein 3)			233	2e-060
	insulin-like growth factor-binding protein 3 precursor [validated] -				
IOHU3	human				
AAA52541.1	insulin-like growth factor-binding protein			233	2e-060
AAA52706.1	growth factor-binding protein-3 precursor			233	2e-060

NM_021501	U: +2.01	CAA46087.1	insulin-like growth factor binding protein 3	233	2e-060
		AAH00013.1	Insulin-like growth factor binding protein 3	233	2e-060
		AAH18962.1	Insulin-like growth factor binding protein 3	233	2e-060
		BAC87023.1	unnamed protein product	213	2e-054
		NP_056981.			
NP_067476	Mm.34428	2	protein inhibitor of activated STAT protein PIASy	844	0
			Protein inhibitor of activated STAT protein gamma (PIAS-gamma)		
		Q8N2W9	(PIASy)	844	0
		AAH29874.1	Protein inhibitor of activated STAT protein PIASy	844	0
		AAH10047.2	PIASy protein	837	0
		AAC36703.1	protein inhibitor of activated STAT protein PIASy	835	0
		AAD45155.1	protein inhibitor of activated STAT	819	0
			protein inhibitor of activated STAT, 1; protein inhibitor of		
		NP_057250.	activated STAT-1; AR interacting protein; DEAD/H		
		1	(Asp-Glu-Ala-Asp/His) box binding protein 1	412	e-114
			Protein inhibitor of activated STAT protein 1 (Gu binding protein)		
			(GBP) (RNA helicase II binding protein) (DEAD/H		
		O75925	box-binding protein 1)	412	e-114
		AAD49722.1	protein inhibitor of activated STAT-1	412	e-114
		AAC36702.1	protein inhibitor of activated STAT protein PIAS1	410	e-114
		JC5517	Gu/RNA helicase II binding protein - human	409	e-114
		AAB58488.1	Gu binding protein	409	e-114
		NP_006090.			
		1	protein inhibitor of activated STAT3	406	e-113
		Q9Y6X2	Protein inhibitor of activated STAT protein 3	406	e-113
		BAA78533.1	protein inhibitor of activated STAT3	406	e-113
		AAH01154.1	protein inhibitor of activated STAT3	406	e-113
		AAH30556.1	protein inhibitor of activated STAT3	406	e-113
		AAP35684.1	protein inhibitor of activated STAT3	406	e-113
				406	e-113

NP_004662.			
1	protein inhibitor of activated STAT X isoform beta	403	e-112
AAC36705.1	protein inhibitor of activated STAT protein PIASx-beta	403	e-112
NP_775298.			
1	protein inhibitor of activated STAT X isoform alpha	403	e-112
AAC36704.1	protein inhibitor of activated STAT protein PIASx-alpha	403	e-112
AAH15190.1	Protein inhibitor of activated STAT X, isoform alpha	403	e-112

Master Tables 101-199

In the related applications set forth at the beginning of the specification, we have looked at differential expression of genes in various organs and tissue with respect to (1) aging, (2) hyperinsulinemia and/or type II diabetes. Master Tables 101-199 (note that some of these table numbers are reserved for future use) tabulate those mouse genes which appear both in Master Table 1 of this application, and in the corresponding table of at least one of the related applications.

The following human proteins are considered to be of particular interest:

Human proteins corresponding to mouse genes listed as favorable both in Master Table 1 and in at least one of Master Tables 101-199, which are not listed as unfavorable in any of Master Tables 101-199; and

Human proteins corresponding to mouse genes listed as unfavorable both in Master Table 1 and in at least one of Master Tables 101-199, which are not listed as favorable in any of Master Tables 101-199.

Master Table 10 Genes Differentially Expressed With Respect to Age in Both Liver and Muscle			
Mouse Gene	Mouse Description	Liver Aging Behavior	Muscle Aging Behavior
AF281045	Mus musculus 2-5A-dependent RNase L mRNA, complete cds	U:4.86 (5to11)	U:+2.12
AF316872	Mus musculus protein kinase BRPK mRNA, complete cds	U:2.16 (YtoM)	U:+2.26 F:3.65
AK015750	AK015750 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930511F10:sulfotransferase, estrogen preferring, full insert sequence	U:2.56 (YtoO)	U:+7.39
AK018226	Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330533H24, full insert sequence	U:4.01 (5to19)	F:2.35
J04694	MUSCOL1A4A Mus musculus alpha-1 type IV collagen (Col4a-1) mRNA, complete cds	F:2.05 (5to11)	F:6.66
NM_007702	Mus musculus cell death-inducing DNA fragmentation factor, alpha subunit-like effector A (Cidea), mRNA	U:52.77 (YtoO)	U:+1.88
NM_007952	Mus musculus glucose regulated protein, 58 kDa (Grp58), mRNA	F:2.65 (5to19)	F:2.59
NM_008161	Mus musculus glutathione peroxidase 3 (Gpx3), mRNA	U:3.13 (YtoO)	U:+2.43
NM_008524	Mus musculus lumican (Lum), mRNA	F:2.41 (5to19)	F:2.01
NM_009075	Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA	U:2.09 (YtoO)	F:2.48
NM_009242	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA	F:2.73 (5to19)	F:4.66
NM_009381	Mus musculus thyroid hormone responsive SPOT14 homolog (Rattus) (Thrsp), mRNA	U:5.69 (YtoO)	F:2.18
NM_010238	Mus musculus bromodomain-containing 2 (Brd2), mRNA	F:2.33 (8to19)	F:2.27
NM_010917	Mus musculus nidogen 1 (Nid1), mRNA	F:2.3 (5to11)	F:2.54
NM_011579	Mus musculus T-cell specific GTPase (Tgtp), mRNA	F:2.1 (5to19)	U:+2.72
NM_016906	Mus musculus SEC61, alpha subunit (S. cerevisiae) (Sec61a), mRNA	F:2.37 (5to19)	U:+2.79 F:3.89

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NM_0197 50	Mus musculus N-acetyltransferase 6 (Nat6), mRNA	F:2.02 (5to19)	F:2.55
NM_0198 24	Mus musculus actin related protein 2/3 complex, subunit 3 (21 kDa) (Arpc3), mRNA	F:5.75 (7to19)	U:+2.14
NM_0213 01	Mus musculus solute carrier family 15 (H+/peptide transporter), member 2 (Slc15a2), mRNA	F:3.08 (YtoM)	F:2.35
NM_0224 34	Mus musculus cytochrome P450, subfamily IVF, polypeptide 14 (leukotriene B4 omega hydroxylase) (Cyp4f14), mRNA	F:2.19 (5to19)	U:+2.12
NM_0231 84	Mus musculus Kruppel-like factor 15 (Klf15), mRNA	F:2.87 (5to11)	U:+2.85 F:4.85
NM_0261 89	Mus musculus RIKEN cDNA 2310005P05 gene (2310005P05Rik), mRNA	U:2.29 (5to11)	U:+2.14
NM_0263 46	Mus musculus RIKEN cDNA 4833442G10 gene (4833442G10Rik), mRNA	F:3.64 (YtoO)	U:+6.12
U89415	MMU89415 Mus musculus strain BALB/c elongation factor 2 mRNA, partial cds	F:2.73 (5to19)	U:+2.02 F:2.92

Master Table 102: Genes Differentially Expressed in Muscle with Respect to (1) Aging and (2) type 1 diabetes and/or hyperinsulinemia			
Accession	Gene Description	Muscle Expression	Muscle Expression
AA510875	vh59b09.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:891257 5' similar to TR:G499130 G499130 ES1 PROTEIN. ;, mRNA sequence	U:(C-IR) 2.21 F:(IR-D) 2.64	U:+2.18
AK017926	Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830413E08, full insert sequence	F:(C-D)2. 38	F:5.21
NM_007702	Mus musculus cell death-inducing DNA fragmentation factor, alpha subunit-like effector A (Cidea), mRNA	U:(C-IR) 2.16	U:+1.88
NM_007995	Mus musculus ficolin A (Fcna), mRNA	U:(C-IR) 2.21 U:(C-D) 2.45	U:+2.2
NM_008302	Mus musculus heat shock protein, 84 kDa 1 (Hsp84-1), mRNA	U:(IR-D) 2.71	U:+2.19
NM_008458	Mus musculus kallikrein binding protein (Klkbp), mRNA	U:(C-D) 2.59	U:+2.04
NM_008687	Mus musculus nuclear factor I/B (Nfib), mRNA	F:(C-IR) 2.69	U:+2.04
NM_009244	Mus musculus serine protease inhibitor 1-2 (Spi1-2), mRNA	U:(IR-D) 2.26	U:+6.8 F:6.19
NM_009349	Mus musculus thioether S-methyltransferase (Temt), mRNA	F:(C-IR) 2.85 U:(IR-D) 3.02	U:+2.01
NM_009464	Mus musculus uncoupling protein 3, mitochondrial (Ucp3), mRNA	F:(IR-D) 2.07	F:2.23
NM_009608	Mus musculus actin, alpha, cardiac (Actc1), mRNA	U:(C-IR) 2.32 F:(C-D) 2.42 F:(IR-D) -5.6	F:15.59
NM_010514	Mus musculus insulin-like growth factor 2 (Igf2), mRNA	F:(IR-D) 2.06	F:2.86
NM_010780	Mus musculus mast cell protease 5 (Mcpt5), mRNA	U:(C-IR) 2.03	U:+2.13
NM_011638	Mus musculus transferrin receptor (Trfr), mRNA	F:(C-D) 2.02	F:2.02

NM_012000	Mus musculus ceroid-lipofuscinosis, neuronal 8 (Cln8), mRNA	F:(IR-D) 2.09	F:2.59
NM_013743	Mus musculus pyruvate dehydrogenase kinase 4 (Pdk4), mRNA	U:(C-IR) 2.15 U:(C-D) 2.04	F:3.21
NM_021282	Mus musculus cytochrome P450, 2e1, ethanol inducible (Cyp2e1), mRNA	F:(C-IR) 2.19 F:(C-D) 2.5	F:2
NM_022314	Mus musculus tropomyosin 3, gamma (Tpm3), mRNA	F:(C-IR) 2.32	U:+2.12
NM_025285	Mus musculus superiorcervical ganglia, neural specific 10 (Scgn10), mRNA	F:(C-IR) 4.72	U:+2.90 F:5.69
NM_025746	Mus musculus RIKEN cDNA 4933415F23 gene (4933415F23Rik), mRNA	U:(C-IR) 2.24	U:+2
NM_026346	Mus musculus RIKEN cDNA 4833442G10 gene (4833442G10Rik), mRNA	U:(IR-D) 2.28	U:+6.12
NM_028784	Mus musculus RIKEN cDNA 1200014I03 gene (1200014I03Rik), mRNA	F:(C-IR) 2.01	F:2.07
U08020	MMU08020 Mus musculus FVB/N collagen pro-alpha-1 type I chain mRNA, complete cds	F:(IR-D) 2.16	F:11.16

Master Table 100: Genes Differentially Expressed in Muscle with respect to Aging and in Pancreas with respect to Type II Diabetes and Hyperinsulinemia			
Mouse Gene	Gene Description	Relative Expression in Muscle	Relative Expression in Pancreas
AB035725	Mus musculus SYNCRIP mRNA, complete cds	F:(C-HI) 3.26 F:(C-D) 2.96	F:2.3
AF064749	AF064749 Mus musculus type VI collagen alpha 3 subunit mRNA, complete cds	U:(C-D) 3.02	F:3.77
AF316872	Mus musculus protein kinase BRPK mRNA, complete cds	F:(C-D) 3.41 F:(C-HI) 2.98	U:+2.26 F:3.65
AK012765	Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810019K23, full insert sequence	F:(C-D) 3.67 F:(C-HI) 3.16	F:2.12
AK015750	AK015750 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930511F10:sulfotransferase, estrogen preferring, full insert sequence	U:(C-HI) 3.54	U:+2.82
NM_007484	Mus musculus aplysia ras-related homolog 9 (RhoC) (Arhc), mRNA	F:(C-D) 3.02	F:2.02
NM_009242	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA	U:(C-D) 3.49	F:4.66
NM_009825	Mus musculus serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1 (Serpinh1), mRNA	F:(C-D) 2.83 F:(C-HI) 2.5	F:3.01
NM_011340	Mus musculus pigment epithelium-derived factor (Pddf), mRNA	F:(C-D) 2.62	F:2.62
NM_011571	Mus musculus testis specific protein kinase 1 (Tesk1), mRNA	F:(C-D) 2.56	U:+2.10 F:2.85
NM_011817	Mus musculus growth arrest and DNA-damage-inducible, gamma (Gadd45g), mRNA	F:(C-D) 2.52 F:(C-HI) 3.43	F:2.93
NM_011829	Mus musculus inosine 5'-phosphate dehydrogenase 1 (Impdh1), mRNA	F:(C-D) 2.57	U:+2.31 F:4.38
NM_016906	Mus musculus SEC61, alpha subunit (S. cerevisiae) (Sec61a), mRNA	F:(C-D) 5.39	U:+2.79 F:3.89
NM_019649	Mus musculus cleft lip and palate associated transmembrane protein 1 (Clptm1), mRNA	F:(C-D) 2.86	F:2.17

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NM_021301	Mus musculus solute carrier family 15 (H ⁺ /peptide transporter), member 2 (Slc15a2), mRNA	U:(C-HI) 2.8	F:2.35
NM_022417	Mus musculus integral membrane protein 3 (Itm3-pending), mRNA	F:(C-D) 2.58 F:(C-HI) 2.6	F:2.57
NM_026189	Mus musculus RIKEN cDNA 2310005P05 gene (2310005P05Rik), mRNA	U:(C-D) 3.66 U:(C-HI) 2.51	U:+2.14
NM_031388	Mus musculus ubiquitin specific protease 26 (Usp26), mRNA	U:(C-D) 3.08	U:+2.13
U89415	MMU89415 Mus musculus strain BALB/c elongation factor 2 mRNA, partial cds	F:(C-D) 3.45 F:(C-HI) 2.58	U:+2.02 F:2.92

Master Table 10: Genes Differentially Expressed both in Muscle with respect to Aging and in Liver with respect to Type II Diabetes and/or Hyperlipidemia

Muscle Gene	Muscle Description	Liver Diabetes Behavior	Muscle Aging Behavior
AK007378	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810008K03:related to CG10365 PROTEIN, full insert sequence	U:(C-IR) 2.77	U:+2.36
AK013885	Mus musculus 12 days embryo head cDNA, RIKEN full-length enriched library, clone:3010002G07, full insert sequence	U:(C-D)+ 4.18	F:3.16
AK018226	Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330533H24, full insert sequence	F:(C-IR) 2.53, F:(C-D) 2.4	F:2.35
NM_007679	Mus musculus CCAAT/enhancer binding protein (C/EBP), delta (Cebpd), mRNA	U:(C-IR) 2.11	F:2.11
NM_007702	Mus musculus cell death-inducing DNA fragmentation factor, alpha subunit-like effector A (Cidea), mRNA	U:(C-D)4 .7	U:+1.88
NM_007743	Mus musculus procollagen, type I, alpha 2 (Col2a2), mRNA	U:(C-D) 2	F:7.82
NM_009349	Mus musculus thioether S-methyltransferase (Temt), mRNA	F:(C-D) 2.04	U:+2.01
NM_009425	Mus musculus tumor necrosis factor (ligand) superfamily, member 10 (Tnfsf10), mRNA	F:(IR-D) 10.21	F:2.06
NM_009964	Mus musculus crystallin, alpha B (Cryab), mRNA	U:(IR-D) 2.06	U:+2.06 F:-2.12
NM_011579	Mus musculus T-cell specific GTPase (Tgtp), mRNA	U:(C-IR) 2.13 F:(C-D) 2.1	U:+2.72
NM_011817	Mus musculus growth arrest and DNA-damage-inducible, gamma (Gadd45g), mRNA	F:(C-IR) 2.13	F:2.93
NM_013703	Mus musculus very low density lipoprotein receptor (Vldlr), mRNA	U:(C-D) 3.61	U:+2.61
NM_013743	Mus musculus pyruvate dehydrogenase kinase 4 (Pdk4), mRNA	F:(C-IR) 2.19	F:3.21
NM_023184	Mus musculus Kruppel-like factor 15 (Klf15), mRNA	U:(C-IR) 2.34	U:+2.85 F:-4.85
NM_053200	Mus musculus carboxylesterase 3 (Ces3), mRNA	F:(C-IR) 2.04	U:+2.08

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The appended claims are to be treated as a non-limiting recitation of preferred embodiments.

In addition to those set forth elsewhere, the following references are hereby incorporated by reference, in their most recent editions as of the time of filing of this application: Kay, Phage Display of Peptides and Proteins: A Laboratory Manual; the John Wiley and Sons Current Protocols series, including Ausubel, Current Protocols in Molecular Biology; Coligan, Current Protocols in Protein Science; Coligan, Current Protocols in Immunology; Current Protocols in Human Genetics; Current Protocols in Cytometry; Current Protocols in Pharmacology; Current Protocols in Neuroscience; Current Protocols in Cell Biology; Current Protocols in Toxicology; Current Protocols in Field Analytical Chemistry; Current Protocols in Nucleic Acid Chemistry; and Current Protocols in Human Genetics; and the following Cold Spring Harbor Laboratory publications: Sambrook, Molecular Cloning: A Laboratory Manual; Harlow, Antibodies: A Laboratory Manual; Manipulating the Mouse Embryo: A Laboratory Manual; Methods in Yeast Genetics: A Cold Spring Harbor Laboratory Course Manual; Drosophila Protocols; Imaging Neurons: A Laboratory Manual; Early Development of *Xenopus laevis*: A Laboratory Manual; Using

Antibodies: A Laboratory Manual; At the Bench: A Laboratory Navigator; Cells: A Laboratory Manual; Methods in Yeast Genetics: A Laboratory Course Manual; Discovering Neurons: The Experimental Basis of Neuroscience; Genome Analysis: A Laboratory Manual Series ; Laboratory DNA Science; Strategies for Protein Purification and Characterization: A Laboratory Course Manual; Genetic Analysis of Pathogenic Bacteria: A Laboratory Manual; PCR Primer: A Laboratory Manual; Methods in Plant Molecular Biology: A Laboratory Course Manual ; Manipulating the Mouse Embryo: A Laboratory Manual; Molecular Probes of the Nervous System; Experiments with Fission Yeast: A Laboratory Course Manual; A Short Course in Bacterial Genetics: A Laboratory Manual and Handbook for Escherichia coli and Related Bacteria; DNA Science: A First Course in Recombinant DNA Technology; Methods in Yeast Genetics: A Laboratory Course Manual; Molecular Biology of Plants: A Laboratory Course Manual.

All references cited herein, including journal articles or abstracts, published, corresponding, prior or otherwise related U.S. or foreign patent applications, issued U.S. or foreign patents, or any other references, are entirely incorporated by reference herein, including all data, tables, figures, and text presented in the cited references. Additionally, the entire contents of the references cited within the references cited herein are also entirely incorporated by reference.

Reference to known method steps, conventional methods steps, known methods or conventional methods is not in any way an admission that any aspect, description or embodiment of the present invention is disclosed, taught or suggested in the relevant art.

The foregoing description of the specific embodiments will so fully reveal the general nature of the invention that others can, by applying knowledge within the skill of the

art (including the contents of the references cited herein), readily modify and/or adapt for various applications such specific embodiments, without undue experimentation, without departing from the general concept of the present invention. Therefore, such adaptations and modifications are intended to be within the meaning and range of equivalents of the disclosed embodiments, based on the teaching and guidance presented herein. It is to be understood that the phraseology or terminology herein is for the purpose of description and not of limitation, such that the terminology or phraseology of the present specification is to be interpreted by the skilled artisan in light of the teachings and guidance presented herein, in combination with the knowledge of one of ordinary skill in the art.

Any description of a class or range as being useful or preferred in the practice of the invention shall be deemed a description of any subclass (e.g., a disclosed class with one or more disclosed members omitted) or subrange contained therein, as well as a separate description of each individual member or value in said class or range.

The description of preferred embodiments individually shall be deemed a description of any possible combination of such preferred embodiments, except for combinations which are impossible (e.g, mutually exclusive choices for an element of the invention) or which are expressly excluded by this specification.

If an embodiment of this invention is disclosed in the prior art, the description of the invention shall be deemed to include the invention as herein disclosed with such embodiment excised.

Introduction to Master Tables

The master tables reflect applicants' analysis of the gene chip data.

For each probe corresponding to a differentially expressed mouse gene, Master Table 1 identifies

Col. 1: The mouse gene (upper) and mouse protein (lower) database accession #s.

Col. 2: The corresponding mouse Unigene Cluster, as of the 4th Quarter 2001 build.

Col. 3: The behavior (differential expression) observed for the mouse gene. This column identifies the gene as favorable(F) or unfavorable (U) on the basis of its differential behavior in the comparisons (older vs. younger). As more than one older vs. younger comparison is made, only the result of the comparison yielding the greatest differential is listed. In the case of a gene with mixed behavior, both the result of the comparison yielding the greatest favorable differential and the result of the comparison yielding the greatest unfavorable differential are listed.

One possible way of characterizing the degree of differential expression for a particular comparison would be to take the ratio of older to younger. If that ratio is at least 2:1, the behavior is considered unfavorable, and if it is not more than 0.5:1, it is unfavorable.

Use of an older/younger ratio is awkward when one wants to compare the degree of differential expression without regard

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to the direction of change. Consequently, in the Master Table, the numerical value is the ratio of the greater value to the lesser value. If this ratio is at least two fold, the degree of differential expression is considered significant.

In some of the related applications cited above, and perhaps occasionally in this application, a ratio may be given as a negative number. This does not have its usual mathematical meaning; it is merely a flag that in the comparison, the older value was less than the younger one, i.e., the gene was favorable. For the purpose of applying the teachings of the specification concerning desired ratios, any negative value should be converted to a positive one by taking its absolute value.

Col. 4: A related human protein, identified by its database accession number. Usually, several such proteins are identified relative to each mouse gene. These proteins have been identified by BLAST searches, as explained in cols. 6-7.

Col. 5: The name of the related human protein.

Col. 6: The score (in bits) for the alignment performed by the BLAST program.

Col. 7: The E-value for the alignment performed by the BLAST program. It is worth noting that Unigene considers a Blastx E Value of less than $1e-6$ to be a "match" to the reference sequence of a cluster.

Unless otherwise indicated, the bit score and E-value for the alignment is with respect to the alignment of the mouse

DNA of col. 1 to the human protein of col. 4 by BlastX, according to the default parameters.

Master Table 1 is divided into three subtables on the basis of the Behavior" in col. 3. If a gene has at least one favorable behavior, and no unfavorable ones, it is put into Subtable 1A. In the opposite case, it is put into Subtable 1B. If its behavior is mixed, i.e., at least one favorable and at least one unfavorable, it is put into Subtable 1C. (If no subtable 1C appears below, then no genes had mixed behavior which satisfied the minimum two-fold difference requirement.)

The corresponding human gene clusters are also of interest. These may be obtained in a number of ways. First, one may search on Unigene

(<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=unigene>) for the identified human protein. Review the "hits" (each of which is a Unigene record) for those prefixed by "Hs."

Secondly, one may access the Unigene record for the mouse gene cluster (which is given in Master Table 1), and then click on "Homologene". This will bring up a new page which includes the section "Possible Homologous Genes". One of the entries should be a Homo sapiens gene (considered by Unigene to be the most related human gene); click on its Unigene record link.

Additional information of interest may be accessed by searching with the mouse gene accession # in the Mouse Gene Informatics database, at <http://www.informatics.jax.org/>.

The related applications may contain reference to "2-16 week old mice". In the anti-diabetes series of applications, 3 week mice were put on a diet to induce obesity, hyperinsulinemia and diabetes. The 2-16 week old mice were more accurately described as mice who had been on that diet for 2-16 weeks, i.e., they were actually 5-19

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weeks (35-133 days) old. Even some of the anti-aging series of applications made reference to 2-16 week old mice, even though the mice were in fact 5-19 weeks (35-133 days) old.

5 (1) an antagonist of a polypeptide, occurring in said subject,
which is substantially structurally identical or
conservatively identical in sequence to a reference protein
which is selected from the group consisting of mouse and human
proteins set forth in master table 1, subtables 1B or 1C,

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(2) an anti-sense vector which inhibits expression of said
polypeptide in said subject,

where said agent reduces a rate of biological aging in said
15 subject, and/or delays the time of onset, or reduces the
severity, of an undesirable age-related phenotype in said
subject, and/or protects against an age-related disease.

3. A method of determining a biological age of a human
20 subject, or a rate of biological aging of a human subject,
which comprises

assaying tissue or body fluid samples from said subjects to
determine the level of expression of a "favorable" human marker
25 gene, said human marker gene encoding a human protein which is
substantially structurally identical or conservatively
identical in sequence to a reference protein which is selected
from the group consisting of mouse and human proteins set
forth in master table 1, subtables 1A or 1C ,

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and inversely correlating the level of expression of said
marker gene with a biological age or a rate of biological
aging of said patient.

35 4. A method of determining a biological age of a human
subject, or a rate of biological aging of a human subject,
which comprises

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assaying tissue or body fluid samples from said subjects to determine the level of expression of an "unfavorable" human marker gene, said human marker gene encoding a human protein which is substantially structurally identical or

10 conservatively identical in sequence to a reference protein which is selected from the group consisting of mouse and human proteins set forth in master table 1, subtables 1B or 1C,

15 and directly correlating the level of expression of said marker gene with a biological age or a rate of biological aging of said subject.

5. The method of claims 1 or 2 in which (I) applies.

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6. The method of claims 1 or 2 in which (II) applies.

7. The method of claims 1 or 2 in which (III) applies.

25 8. The method of claims 3 or 4 in which the level of expression of the marker gene is ascertained by measuring the level of the corresponding messenger RNA.

9. The method of claims 3 or 4 in which the level of
30 expression is ascertained by measuring the level of a protein encoded by said marker gene.

10. The method of any one of claims 1-9 in which the reference protein is a human protein.

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11. The method of claim 10 in which the E-value cited for the BlastX alignment of the reference human protein in Master Table 1 to the corresponding reference mouse DNA in Master Table 1 is not more than e-60.

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- 5 12. The method of claim 10 in which the E-value cited for the BlastX alignment of the reference human protein in Master Table 1 to the corresponding reference mouse DNA in Master Table 1 is not more than e^{-70} .
- 10 13. The method of claim 10 in which the E-value cited for the BlastX alignment of the reference human protein in Master Table 1 to the corresponding reference mouse DNA in Master Table 1 is not more than e^{-80} .
- 15 14. The method of any one of claims 1-9 in which the reference protein is a mouse protein.
15. The method of any one of claims 1-14 in which said
20 polypeptide is at least 80% identical or at least highly conservatively identical to said reference protein.
16. The method of any one of claims 1-14 in which said
25 polypeptide is at least 90% identical to said reference protein.
17. The method of any one of claims 1-14 in which said
polypeptide is at least 95% identical to said reference
protein.
- 30 18. The method of any one of claims 1-14 in which said polypeptide is identical to said reference protein, or differs from it by not more than a single amino acid substitution.
- 35 19. The method of claim 18 in which said polypeptide is identical to said reference protein.
20. The method of claims 2 or 4, or of any of claims 5-19 to the extent dependent on 2 or 4, in which the antagonist is an
40 antibody, or an antigen-specific binding fragment of an

5 antibody.

21. The method of claims 2 or 4, or of any of claims 5-19 to
the extent dependent on 2 or 4, in which the antagonist is a
peptide, peptoid, nucleic acid, or peptide nucleic acid
10 oligomer.

22. The method of claims 2 or 4, or of any of claims 5-19 to
the extent dependent on 2 or 4, in which the antagonist is an
organic molecule with a molecular weight of less than 500
15 daltons.

23. The method of claim 22 in which said organic molecule is
identifiable as a molecule which binds said polypeptide by
screening a combinatorial library.

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24. The method of claims 1 or 2, or of any one of claims 5-23
to the extent dependent on 1 or 2, which further comprises
administration of an antagonist of CIDE-A.

25 25. The method of claim 5 in which biological age is measured
by a biomarker.

26. The method of claim 25 in which at least one marker is the
level of a biochemical in the blood of the subject.

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27. The method of claim 26 in which the biochemical is growth
hormone or IGF-1.

28. The method of claim 25 in which the marker is a simple
35 biomarker.

29. The method of claim 25 in which the marker is a composite
biomarker.

40 30. The method of claim 5 in which the affected biological age

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5 is the overall biological age of the subject.

31. The method of claim 5 in which the affected biological age is the biological age of a body system of the subject.

10 32. The method of claim 5 in which the affected biological age is the biological age of an organ or tissue of the subject.

33. The method of claim 32 in which the organ or tissue is a muscle.

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34. The method of claim 32 in which the organ or tissue is a skeletal muscle.

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35. The method of claim 32 in which the organ or tissue is the gastrocnemius muscle.

36. The method of claims 1 or 3, or of any of the other preceding claims to the extent dependent on 1 or 3, where the reference protein is listed in subtable 1A.

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37. The method of claims 2 or 4, or of any of the other preceding claims to the extent dependent on 1 or 3, where the reference protein is listed in subtable 1B.

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38. Use of a protective amount of an agent which is

(1) a polypeptide which is substantially structurally identical or conservatively identical in sequence to a reference protein which is selected from the group consisting of mouse and human proteins set forth in master table 1, subtables 1A or 1C,

or

(2) an expression vector encoding the polypeptide of (1) above and expressible in a human cell, under conditions conducive to expression of the polypeptide of (1);

where said agent reduces a rate of biological aging in a subject, and/or delays the time of onset, or reduces the severity, of an undesirable age-related phenotype in said subject, and/or protects against an age-related disease,

in the manufacture of a composition for (I) reducing a rate of biological aging in a human subject, and/or (II) delaying the time of onset, or reducing the severity, of an undesirable age-related phenotype, and/or (III) protecting against an age-related (senescent) disease.

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39. Use of a protective amount of an agent which is

(1) an antagonist of a polypeptide, occurring in said subject, which is substantially structurally identical or conservatively identical in sequence to a reference protein which is selected from the group consisting of mouse and human proteins set forth in master table 1, subtables 1B or 1C,

(2) an anti-sense vector which inhibits expression of said polypeptide in said subject,

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where said agent reduces a rate of biological aging in said subject, and/or delays the time of onset, or reduces the severity, of an undesirable age-related phenotype in said subject, and/or protects against an age-related disease,

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in the manufacture of a composition for (I) reducing a rate of biological aging in a human subject, and/or (II) delaying the time of onset, or reducing the severity, of an undesirable age-related phenotype, and/or (III) protecting against an age-related (senescent) disease.

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40. A method of determining a biological age of a human subject, or a rate of biological aging of a human subject, which comprises

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assaying tissue or body fluid samples from said subjects to determine the level of expression of a "favorable" human marker gene, said human marker gene encoding a human protein which is substantially structurally identical or conservatively identical in sequence to a reference protein which is selected from the group consisting of mouse and human proteins set forth in master table 1, subtables 1A or 1C ,

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and inversely correlating the level of expression of said marker gene with a biological age or a rate of biological aging of said patient.

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41. A method of determining a biological age of a human subject, or a rate of biological aging of a human subject, which comprises

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assaying tissue or body fluid samples from said subjects to determine the level of expression of an "unfavorable" human marker gene, said human marker gene encoding a human protein which is substantially structurally identical or

10 conservatively identical in sequence to a reference protein which is selected from the group consisting of mouse and human proteins set forth in master table 1, subtables 1B or 1C,

15 and directly correlating the level of expression of said marker gene with a biological age or a rate of biological aging of said subject.

42. The use of claims 38 or 39 in which (I) applies.

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43. The use of claims 38 or 39 in which (II) applies.

44. The use of claims 38 or 39 in which (III) applies.

25 45. The method of claims 40 or 41 in which the level of expression of the marker gene is ascertained by measuring the level of the corresponding messenger RNA.

46. The method of claims 40 or 41 in which the level of
30 expression is ascertained by measuring the level of a protein encoded by said marker gene.

47. The use or method of any one of claims 38-46 in which the reference protein is a human protein.

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48. The use or method of claim 47 in which the E-value cited for the BlastX alignment of the reference human protein in Master Table 1 to the corresponding reference mouse DNA in Master Table 1 is not more than e^{-60} .

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- 5 49. The method of claim 47 in which the E-value cited for the BlastX alignment of the reference human protein in Master Table 1 to the corresponding reference mouse DNA in Master Table 1 is not more than e-70.
- 10 50. The method of claim 47 in which the E-value cited for the BlastX alignment of the reference human protein in Master Table 1 to the corresponding reference mouse DNA in Master Table 1 is not more than e-80.
- 15 51. The use or method of any one of claims 38-46 in which the reference protein is a mouse protein.
52. The use or method of any one of claims 38-51 in which said
20 polypeptide is at least 80% identical or at least highly conservatively identical to said reference protein.
53. The use or method of any one of claims 38-51 in which said
25 polypeptide is at least 90% identical to said reference protein.
54. The use or method of any one of claims 38-51 in which said
polypeptide is at least 95% identical to said reference
protein.
- 30 55. The use or method of any one of claims 38-51 in which said polypeptide is identical to said reference protein, or differs from it by not more than a single amino acid substitution.
- 35 56. The use or method of claim 55 in which said polypeptide is identical to said reference protein.
57. The use or method of claims 38 or 40, or of any of claims
42-56 to the extent dependent on 38 or 40, in which the
40 antagonist is an antibody, or an antigen-specific binding

5 fragment of an antibody.

58. The use or method of claims 38 or 40, or of any of claims
42-56 to the extent dependent on 38 or 40, in which the
antagonist is a peptide, peptoid, nucleic acid, or peptide
10 nucleic acid oligomer.

59. The use or method of claims 38 or 40, or of any of claims
42-56 to the extent dependent on 38 or 40, in which the
antagonist is an organic molecule with a molecular weight of
15 less than 500 daltons.

60. The use or method of claim 59 in which said organic
molecule is identifiable as a molecule which binds said
polypeptide by screening a combinatorial library.
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61. The use of claims 38 or 39, or of any one of claims 42-60
to the extent dependent on 38 or 39, which further comprises
administration of an antagonist of CIDE-A.

25 62. The method of claim 41 in which biological age is measured
by a biomarker.

63. The method of claim 62 in which at least one marker is the
level of a biochemical in the blood of the subject.
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64. The method of claim 63 in which the biochemical is growth
hormone or IGF-1.

65. The method of claim 62 in which the marker is a simple
35 biomarker.

66. The method of claim 62 in which the marker is a composite
biomarker.

40 67. The method of claim 42 in which the affected biological

5 age is the overall biological age of the subject.

68. The method of claim 42 in which the affected biological age is the biological age of a body system of the subject.

10 69. The method of claim 42 in which the affected biological age is the biological age of an organ or tissue of the subject.

15 70. The method of claim 69 in which the organ or tissue is a muscle.

71. The method of claim 70 in which the organ or tissue is a skeletal muscle.

20 72. The method of claim 71 in which the organ or tissue is the gastrocnemius muscle.

25 73. The use or method of claims 38 or 40, or of any of the other preceding claims to the extent dependent on 38 or 40, where the reference protein is listed in subtable 1A.

74. The use or method of claims 39 or 41, or of any of the other preceding claims to the extent dependent on 39 or 41, where the reference protein is listed in subtable 1B.